

GenCore version 5.1.6
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OM protein - protein search, using sw mode!

Run on: July 28, 2004, 08:49:47 ; Search time 37.771 Seconds
(without alignments)

Sequence: 1 LHFDQYREQLIARVTSVEV.....HLIMELWEKGSKGGIPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 31551802 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_rabbit:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Title:	US-09-996-617-2_COPY_1335_1429
Perfect score:	490
Sequence:	1 LHFDQYREQLIARVTSVEV.....HLIMELWEKGSKGGIPLSS 95
Scoring table:	BLOSUM62
Scoring table:	Gapop 10.0 , Gapext 0.5
Searched:	1017041 segs, 31551802 residues
Total number of hits satisfying chosen parameters:	1017041
Minimum DB seq length:	0
Maximum DB seq length: <td>2000000000</td>	2000000000
Post-processing:	Minimum Match 0%
Maximum Match 100%	
Listing first 45 summaries	

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7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_rabbit:*

13: sp_vertebrate:*

14: sp_unclassified:*

Query Match	16.8% ; Score 82.5; DB 16;	Length 614;	RX MEDLINE=22313464; PubMed=12426347;
Best Local Similarity	26.4% ; Pred. No. 4.3;		RA Weightman A.J., Topping A.W., Hill K.B., Lee L.;
Matches	29; Conservative 20; Mismatches 28;	Indels 33; Gaps 6;	RT "Investigation of two evolutionarily unrelated halocarboxylic acid dehalogenase gene families";
QY	15 VTSVEVVLKLGH----QVLSQEVYERVENT-----PSOMRKLFSLSQSWSW-	58	RL J. Bacteriol. 184:6581-6591 (2002).
Db	404 IRSLSRISLHLGDKWERKEDLESYVQEIQSTAAETPPLDGEDKIDAKERELFYLMQWF	463	DR EMBL; AJ534881; CAD591331; -.
QY	59 -----DRKCDGlyQALKETHP---HLIMEL----W5----KGSKIGLL 91		DR GO; GO:0003677; F:DNA binding; IEA.
Db	464 MSQQLDRDRMSMGAASLVEVRPFADHRILVEYWNIPWDIKWNGHERRIL 513		DR GO; GO:0004833; F:transposase activity; IEA.
RESULT 5			
Q8GVIVI	PRELIMINARY;	PRT;	Length 260;
ID	O8GVIVI	PRT;	260 AA.
AC	Q8GVIVI_;	PRT;	260 AA.
DT	01-MAR-2003 (TREMBLrel. 23, Created)	PRT;	Length 260;
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	PRT;	Length 260;
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	PRT;	Length 260;
DE	Putative transposase (Fragment).	PRT;	Length 260;
GN	TNPA.	PRT;	Length 260;
OS	Pseudomonas sp. F12.	PRT;	Length 260;
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	PRT;	Length 260;
OC	Pseudomonadaceae; Pseudomonas.	PRT;	Length 260;
OX	NCBI_TaxID=217730;	PRT;	Length 260;
RN	[1]	PRT;	Length 260;
RP	SEQUENCE FROM N.A.	PRT;	Length 260;
RC	STRAIN=F12;	PRT;	Length 260;
RA	Hill K.E., Weightman A.J.;	PRT;	Length 260;
RT	"Horizontal transfer of dehalogenase genes on IncP-beta plasmids during bacterial adaptation to degrade alpha-halocarboxylic acids.";	PRT;	Length 260;
RT	Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.	PRT;	Length 260;
RL	EMBL; AJ534880; CAD59131.1; -.	PRT;	Length 260;
DR	GO; GO:0003677; F:DNA binding; IEA.	PRT;	Length 260;
DR	GO; GO:0004803; F:transposase activity; IEA.	PRT;	Length 260;
DR	GO; GO:0006310; P:DNA recombination; IEA.	PRT;	Length 260;
DR	InterPro; IPR002560; Transposase_12.	PRT;	Length 260;
DR	Pfam; PF01610; Transposase_12; 1.	PRT;	Length 260;
FT	NON TER 1	PRT;	Length 260;
FT	NON TER 260	PRT;	Length 260;
SEQ	SEQUENCE 260 AA; 30910 MW;	PRT;	Length 260;
RC	SEQUENCE FROM N.A.	PRT;	Length 260;
RC	STRAIN=142;	PRT;	Length 260;
RC	MEDLINE=9940444; PubMed=10224014;	PRT;	Length 260;
RC	Tsoi T.V., Plotnikova E.G., Cole J.R., Guerin W.F., Bagdasarian M.,	PRT;	Length 260;
RA	Tiedje J.M.;	PRT;	Length 260;
RA	"Cloning, expression, and nucleotide sequence of the Pseudomonas aeruginosa 14 ohb genes coding for oxygenolytic ortho dehalogenation of halobenzoates".	PRT;	Length 260;
RT	Appl. Environ. Microbiol. 65:2151-2162 (1999).	PRT;	Length 260;
RT	DR EMBL; AF121970; AAD20008.1; -.	PRT;	Length 260;
DR	GO; GO:0003677; F:DNA binding; IEA.	PRT;	Length 260;
DR	GO; GO:0004803; F:transposase activity; IEA.	PRT;	Length 260;
DR	InterPro; IPR002560; Transposase_12.	PRT;	Length 260;
DR	Pfam; PF01610; Transposase_12; 1.	PRT;	Length 260;
SEQ	SEQUENCE 338 AA; 39711 MW;	PRT;	Length 260;
RESULT 7			
Q9Z5V9	PRELIMINARY;	PRT;	Length 338;
ID	Q9Z5V9	PRT;	Length 338 AA.
AC	Q9Z5V9_;	PRT;	Length 338 AA.
DT	01-MAY-1999 (TREMBLrel. 10, Created)	PRT;	Length 338 AA.
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	PRT;	Length 338 AA.
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	PRT;	Length 338 AA.
DE	Putative transposase A.	PRT;	Length 338 AA.
GN	TNPA.	PRT;	Length 338 AA.
OS	Pseudomonas aeruginosa.	PRT;	Length 338 AA.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	PRT;	Length 338 AA.
OC	Pseudomonadaceae; Pseudomonas.	PRT;	Length 338 AA.
OX	NCBI_TaxID=287;	PRT;	Length 338 AA.
RN	[1]	PRT;	Length 338 AA.
RP	SEQUENCE FROM N.A.	PRT;	Length 338 AA.
RC	SEQUENCE FROM N.A.	PRT;	Length 338 AA.
RC	STRAIN=142;	PRT;	Length 338 AA.
RC	MEDLINE=9940444; PubMed=10224014;	PRT;	Length 338 AA.
RC	Tsoi T.V., Plotnikova E.G., Cole J.R., Guerin W.F., Bagdasarian M.,	PRT;	Length 338 AA.
RA	Tiedje J.M.;	PRT;	Length 338 AA.
RA	"Cloning, expression, and nucleotide sequence of the Pseudomonas aeruginosa 14 ohb genes coding for oxygenolytic ortho dehalogenation of halobenzoates".	PRT;	Length 338 AA.
RT	Appl. Environ. Microbiol. 65:2151-2162 (1999).	PRT;	Length 338 AA.
RT	DR EMBL; AF121970; AAD20008.1; -.	PRT;	Length 338 AA.
DR	GO; GO:0003677; F:DNA binding; IEA.	PRT;	Length 338 AA.
DR	GO; GO:0004803; F:transposase activity; IEA.	PRT;	Length 338 AA.
DR	InterPro; IPR002560; Transposase_12.	PRT;	Length 338 AA.
DR	Pfam; PF01610; Transposase_12; 1.	PRT;	Length 338 AA.
SEQ	SEQUENCE 338 AA; 39711 MW;	PRT;	Length 338 AA.
RESULT 8			
Q8G977	PRELIMINARY;	PRT;	Length 338;
ID	Q8G977	PRT;	260 AA.
AC	Q8G977_;	PRT;	260 AA.
DT	01-MAR-2003 (TREMBLrel. 23, Created)	PRT;	Length 338;
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	PRT;	Length 338;
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	PRT;	Length 338;
DE	Putative transposase (Fragment).	PRT;	Length 338;
GN	TNPA.	PRT;	Length 338;
OS	Pseudomas putida.	PRT;	Length 338;
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	PRT;	Length 338;
OC	Pseudomonadaceae; Pseudomonas.	PRT;	Length 338;
OX	NCBI_TaxID=303;	PRT;	Length 338;
RN	[1]	PRT;	Length 338;
RP	SEQUENCE FROM N.A.	PRT;	Length 338;
RC	SEQUENCE FROM N.A.	PRT;	Length 338;

052212	PRELIMINARY;	PRT;	404 AA.	SQ	SEQUENCE	404 AA;	47498 MW;	2B130E43026E5404 CRC64;
AC	052212; 06, Created)			Query Match	16.2%;	Score 79.5-	DB 2;	Length 404;
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			Best Local Similarity	32.1%;	Pred. No. 5.5;		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			Matches	27;	Conservative	9;	Gaps 4;
DE	Putative transposase (TnPA).			Qy	7 YREQQLARVTISVEVYLDKHLGQVLSQEQYERV--	--LAENTRPSQMRKLFLSLSQSWDRCK	63	
GN	TNPA.			Db	186 YRAAVAVLPQARIIVDKFHVRKGRLKPSOSRTRL-----	-KGDRKT-	239	
OS	Pseudomonas putida, and			Qy	64 DGLYQALKETH----PHLIMELW 82			
OS	Serratia marcescens			Db	240 ----ILKRAHEVSDFERLIMETW 258			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			RESULT 9				
OC	Pseudomonadaceae; Pseudomonas.			Q9X7J2				
OX	NCBI_TaxID=303, 615;			ID	Q9X7J2	PRELIMINARY;	PRT;	425 AA.
RN	[1]			AC	Q9X7J2;			
RP	SEQUENCE FROM N.A.			DT	01-NOV-1999 (TREMBLrel. 12, Created)			
RC	SPECIES=P.putida; PLASMID=pWW0;			DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
RA	Created A., Lantibertton L., Williams P.A., Thomas C.M.;			DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
RA	"Complete nucleotide sequence of IncP-9 plasmid pWW0";			DE	Putative transposase.			
RT	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			OS	Pseudomonas stutzeri (Pseudomonas perfectionaria).			
RN	[2]			OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
RP	SEQUENCE FROM N.A.			OC	Pseudomonadaceae; Pseudomonas.			
RC	SPECIES=S.marcescens; PLASMID=R471a;			RN	[1]			
RX	LINE=75096669; PubMed=1039756;			RP	SEQUENCE FROM N.A.			
RA	Hedges R.W., Rodriguez-Lemoine V., Datta N.;			RC	STRAIN=ML;			
RA	"R factors from Serratia marcescens.";			RX	MEDLINE=99140403; PubMed=10223973;			
RL	J. Gen. Microbiol. 86:88-92 (1975).			RA	Bolognesi F., Di Lecce C., Galli B., Barbensi P.;			
RN	[3]			RA	"Activation and inactivation of Pseudomonas stutzeri methylbenzene catabolism pathways mediated by a transposable element."			
RP	SEQUENCE FROM N.A.			RT	catabolism pathways mediated by a transposable element."			
RC	SPECIES=S.marcescens; PLASMID=R471a;			RL	Appl. Environ. Microbiol. 65:1876-1882 (1999).			
RX	LINE=93174815; PubMed=8365028;			DR	EMBL: AJ012352; CAB2636; 1-----			
RA	Ho C., Kulaeva O.I., Levine A.S., Woodgate R.;			DR	GO; GO:0003677; P:DNA binding; IEA.			
RA	"A rapid method for cloning mutagenic DNA repair genes: isolation of			DR	GO; GO:0004803; P:transposase activity; IEA.			
RT	umu-complementing genes from multidrug resistance plasmids R391,			DR	GO; GO:0006310; P:DNA recombination; IEA.			
RT	R446b, and R471a.";			DR	InterPro: IPR02560; Transposase_12.			
RL	J. Bacteriol. 175:3411-3419 (1993).			DR	Pfam: PF01610; Transposase_12; 1.			
RN	[4]			DR	SEQUENCE 425 AA; 49494 MW; 4EB338A74655B6BF CRC64;			
RP	SEQUENCE FROM N.A.			Query Match	16.2%;	Score 79.5-	DB 2;	Length 425;
RC	SPECIES=S.marcescens; PLASMID=R471a;			Best Local Similarity	32.1%;	Pred. No. 5.8;		
RX	LINE=98202721; PubMed=126346;			Matches	27;	Conservative	9;	Gaps 4;
RA	Kulaeva O.I., Koornin E.V., Wootton J.C., Levine A.S., Woodgate R.;			Qy	7 YREQQLARVTISVEVYLDKHLGQVLSQEQYERV--	--LAENTRPSQMRKLFLSLSQSWDRCK	63	
RA	"Unusual insertion element polymorphisms in the promoter and			Db	207 YRAAVAVLPQARIIVDKFHVRKGRLKPSOSRTRL-----	-KGDRKT-	260	
RT	terminator regions of the mucAB-like genes of R471a and R446b.";			Qy	64 DGLYQALKETH----PHLIMELW 82			
RL	Mutat. Res. 397:247-262 (1998).			Db	261 ----ILKRAHEVSDFERLIMETW 279			
RN	[5]			RESULT 10				
RP	SEQUENCE FROM N.A.			Q8ZSQ2				
RC	SPECIES=P.putida; PLASMID=pWW0;			ID	Q8ZSQ2;	PRELIMINARY;	PRT;	193 AA.
RX	LINE=22313164; PubMed=12426347;			AC	Q8ZSQ2;			
RA	Weightman A.J., Topping A.W., Hill K.E., Lee L.I., Sakai K.,			DT	01-MAR-2002 (TREMBLrel. 20, Created)			
RA	Slater J.H., Thomas A.W.;			DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
RT	"Transposition of DEH, a Broad-Host-Range Transposon Flanked by			DT	01-MAR-2003 (TREMBLrel. 24, Last annotation update)			
RT	ISPPu12, in Pseudomonas putida Is Associated with Genomic Rearrangements and Dehalogenase Gene Silencing.";			DE	Hypothetical protein PAR3635.			
RT	J. Bacteriol. 184:1581-1591 (2002).			OS	Pyrobaculum aerophilum.			
DR	EMBL: AJ244068; CA086839.1-----			OC	Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;			
DR	EMBL: AF027668; AAC8523.1-----			OC	Thermoproteaceae; Pyrobaculum.			
DR	EMBL: AF28707; AN05080.1-----			OX	NCBI_TaxID=13773;			
DR	EMBL: AF28707; AN05080.1-----			RN	[1]			
DR	EMBL: AF28707; AN05080.1-----			RP	SEQUENCE FROM N.A.			
DR	EMBL: AF28707; AN05080.1-----			RC	STRAIN=IM2 / ATCC 51768 / DSM 7523;			
DR	EMBL: AF28707; AN05080.1-----			RX	MEDLINE=21664377; PubMed=1172869;			
DR	EMBL: AF28707; AN05080.1-----							

RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Müller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002);
 DR EMBL; AP00993; M41650; 61.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 193 AA; 21824 MW; 2456ADDDEFB35DBA6 CRC64;

Query Match 15.9%; Score 78; DB 17; Length 193;
 Best Local Similarity 27.4%; Pred. No. 3.3;
 Matches 23; Conservative 21; Mismatches 22; Indels 18; Gaps 4;

QY 19 EVVLDKLHQVLSQEYERVLAE----NTRPSQ---MRKLFISQSMDRKCKD-- 64
 DB 101 EGVLEKVNHDLLAVEEAKIADAVSALXNLRGSAEWDAQRIFALIKNDAKIDERA 160

OY 65 GLYQALKETHPHLIMELWKGSKK 88
 DB 161 KLLKAISEPPP---QLINEERGEEK 180

RESULT 11
 Q966F3 PRELIMINARY; PRT; 254 AA.
 ID Q966F3;
 AC Q966F3;
 DT 01-OCT-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein T13G4.6.
 GN T13G4.6.

Caenorhabditis elegans.
 OC Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodriline; Ceanorhabditis.
 OX [1] NCBI_TAXID=6239; RN [1] NCBI_TAXID=6239;

RP SEQUENCE FROM N.A.; STRAIN=Bristol N2; PubMed=9851919;
 RX MEDLINE=99069513; RA None;

RT "The genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 288:2011-2018(1998).
 RN [2] SEQUENCE FROM N.A.; STRAIN=Bristol N2;
 RC Favello T.; RA Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 RL SEQUENCE FROM N.A.; STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 DR WormPep; T13G4.6; CB211B1.1;
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:006810; Pi:transport; IEA.
 DR InterPro; IPR00199; Mitoch carrier.
 DR PROSITE; PS00215; MITOCH CARRIER; 1.
 SQ SEQUENCE 254 AA; 2932 MW; 1CA5AE79479422B7 CRC64;

Query Match 15.9%; Score 78; DB 5; Length 254;
 Best Local Similarity 27.1%; Pred. No. 4.6;
 Matches 26; Conservative 18; Mismatches 42; Indels 10; Gaps 4;

Db 83 GLFQQCXDG--QLRIVHPSENSAQIASHRRGGFP 115

RESULT 12
 Q8K4F9 PRELIMINARY; PRT; 376 AA.
 ID Q8K4F9;
 AC Q8K4F9;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE 2'-5' oligoadenylate synthetase 1B.
 GN OAS1B.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Buteleostomi; Euksaryota; Metazoa; Sciuromorphathi; Murinae; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10980;
 RN RP SEQUENCE FROM N.A.;
 RC STRAIN=MOLD/RK;
 RX MEDLINE=2210363; PubMed=12080145; Zhalin I.B., Stockman B.M., Li Y., Pereygin A.A., Scherbik S.V.; Zhalin I.B., Stockman B.M., Li Y., Brinton M.A.; RT Positional cloning of the murine flavivirus resistance gene.;"
 RA Proc. Natl. Acad. Sci. U.S.A. 99:9322-9327(2002).
 DR MGI; AF418006; AAC75461.1; -.
 DR GO; GO:000800; Casl1b
 DR InterPro; IPR006117; 25A_Synth_2.
 DR InterPro; IPR006116; 25A_Synth_UB.
 DR InterPro; IPR001201; PAP_25A_core.
 DR PROSITE; PS0083; 25A_SYNTH_2.
 DR PROSITE; PS50152; 25A_SYNTH_3; 1.
 SQ SEQUENCE 376 AA; 43919 MW; CP34CABC3874842 CRC64;

Query Match 15.8%; Score 77.5; DB 11; Length 376;
 Best Local Similarity 28.3%; Pred. No. 8.2;
 Matches 26; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 1 LHFVDQYREQLIARYTTSVEVLDKLHGQVLSQEYERVLAEENTRPSQMRKLFISLSQSWDR 60
 DB 155 INITLKPNQFYANLISGRTPLGK-EGKLUTCFMGRKYFLNCPTKLRLRLVTHWYQ 213

QY 61 KCKDGLYQALKETHPHLIMEL---WEKGSK 87
 DB 214 LCKERKLGDPLP---PQYALELLTVAYEWYGR 242

RESULT 13
 Q921F0 PRELIMINARY; PRT; 376 AA.
 ID Q921F0;
 AC Q921F0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Similar to 2'-5' oligoadenylate synthetase 1B (2'-5'-oligoadenylate synthetase 1).
 DE OAS1A OR OAS1.
 OS Mus musculus (Mouse), and
 OS Mus musculus (eastern European house mouse).
 OC Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Buteleostomi; Euksaryota; Metazoa; Sciuromorphathi; Murinae; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10980; 39442;
 RN RP SEQUENCE FROM N.A.;
 RC SPECIES=Mouse;
 RA Strubiger R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 [2] RN RP SEQUENCE FROM N.A.;
 RC SPECIES=M.musculus; STRAIN=MBT/Pas;
 RX MEDLINE=22177231; PubMed=2186974;
 RA Mashimo T., Lucas M., Simon-Chazottes D., Frenkiel M.P.,

QY 61 ---KCKDGLYQALKETHPHL-INELWEKGSKKGLP 92

RA Montagutelli X., Ceccaldi P.E., Deubel V., Guenot J.L., Despres P.;
 RT "A non-sense mutation in the gene encoding 2',-5'-oligoadenylate
 synthetase/LI isoform is associated with West Nile virus
 susceptibility in laboratory mice.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:11311-11316 (2002).
 DR EMBL; BC012877; AAH12877; 1.; -.
 DR EMBL; AF46823; AAH97604; 1.; -.
 DR MGD:2180860; Oasia GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:003723; F:RNA binding; IEA.
 DR GO; GO:0016740; F:Transferase activity; IEA.
 DR GO; GO:0006955; P:Immune response; IEA.
 DR InterPro; IPR006117; 25A_SYNTH_2.
 DR InterPro; IPR006116; 25A_SYNTH_core.
 DR InterPro; IPR001201; PAP_25A_core.
 DR PROSITE; PS50152; 25A_SYNTH_2; 1.
 DR PROSITE; PS50152; 25A_SYNTH_3; 1.
 SQ SEQUENCE 376 AA; 43934 MW; 30F970452408FB7E CRC64;
 Query Match 15 8%; Score 77 5; DB 11; Length 376;
 Best Local Similarity 28.3%; Pred. No. 8.2;
 Matches 26; Conservative 17; Mismatches 40; Indels 9; Gaps 3;
 Qy 1 LHPDVOREQLIARTSVVVVLDKLHGQVLSQEYERVLAAENTRPSQRKLFSLSQSWR 60
 Db 155 INTLKPPQFYANLISGRLPLGK-EGKLTCFMGLRKYFLNCEPTKLRLHLVTHQ 213
 Qy 61 KCKDGLYQALKETHPHLIMEL----WEGSK 87
 Db 214 LCKERKGDPPLP---FQYALELLTVYAWEVGSR 242
 RESULT 14
 ID Q95Q18 PRELIMINARY; PRT; 295 AA.
 AC Q95Q18;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Y53FB.39 protein.
 GN Y53FB.39.
 OC Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 Rhabditidae; Peloderaidae; Caenorhabditis.
 NCBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
 RX none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for
 investigating biology.";
 Science 282:2012-2018 (1998).
 EMBL; AL132949; CAB61094; 1.
 DR WormBase; Y53FB.39; CE2418.
 DR InterPro; IPR001279; Blactmase-like.
 DR Pfam; PF00753; lactamase_B; 1.
 SQ SEQUENCE 295 AA; 33102 MW; 5D798FC5C67B97C CRC64;
 Query Match 15 5%; Score 76; DB 5; Length 295;
 Best Local Similarity 26.7%; Pred. No. 8.8;
 Matches 23; Conservative 1; Mismatches 40; Indels 6; Gaps 2;
 Qy 4 VDOYREQLIARTSVVVVLDKLHGQVLSQEYERVLAAENTRPSQRKLFSLSQSWR 63
 Db 206 VDEYEEHRMGREREIJKVLRHEEITMSMVNTQVYADPWAVERLAANINVKLVKLCK 264
 Qy 64 DGLYQALKETHPHLIMELWKGSKKG 89.
 Db 265 DGvVE---NPHEFETKNIGSSSG 285

Search completed: July 28, 2004, 08:54:45
 Job time : 39.771 secs

GenCore version 5.1.6	P11928	mus musculu	
Copyright (C) 1993 - 2004 Compugen Ltd.	P81177	staphylococc	
M protein search, using sw model!	Q8ds85	streptococc	
on on:	Q61645	mus musculu	
July 28, 2004, 08:46:37 ; Search time 9.15663 Seconds (without alignments)	P32534	human parai	
540.228 Million cell updates/sec	P58801	mus musculu	
title: US-09-996-617-2_COPY_1335_1429	Q90660	gallus galli	
perfect score: 490	P27986	homo sapien	
sequence: 1 LHFTDQREQQLIARVTISVEV.....HLIMELWERGSKICCLLPLSS 95	Q9TAH	spiroplasma	
scoring table: BLOSUM62	Q83269	treponema p	
Gapop 10.0 , Gapext 0.5	Q9pb1	campylobact	
searched: 141681 seqs, 52070155 residues	P39057	anthocidari	
Total number of hits satisfying chosen parameters: 141681.	ALIGNMENTS		
DB seq length: 0	RESULT 1		
Maximum DB seq length: 2000000000	NAL1_HUMAN	STANDARD; PRT; 1473 AA;	
Post-processing: Minimum Match 0%	ID NAL1_HUMAN	Q9BZ28; Q9HAV8; Q9UFT4; Q9Y2E0;	
Maximum Match 100%	AC Q9BZ28	Created)	
Listing first 45 summaries	DT 16-OCT-2001 (Rel. 40, Last sequence update)	DT 16-OCT-2001 (Rel. 40, Last sequence update)	
Database : SwissProt_42:*	DT 10-OCT-2003 (Rel. 42, Last annotation update)	DT 10-OCT-2003 (Rel. 42, Last annotation update)	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	DE NACHT_	LRR- and PYD-containing Protein 2 (Death effector filament-forming dcd-4-like apoptosis protein) (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain protein 7).	
SUMMARIES	DB NA0P1 OR DEFCAF_P OR NAC OR CARD7 OR KIAA0926.	GN NALP1 OR DEFCAF_P OR NAC OR CARD7 OR KIAA0926.	
Result No.	Score	Query Match Length DB ID Description	
1	490	100.0 1473 1 NAL1_HUMAN	Q9C000 homo sapien
2	253	51.6 193 1 ASC_MOUSE	Q9epb4 mus musculu
3	236	48.2 195 1 ASC_HUMAN	Q9i1z3 homo sapien
4	96	19.6 203 1 ASC_BRAE	Q919n6 brachydanio
5	94.5	19.3 431 1 CARB_HUMAN	Q92922 homo sapien
6	75	15.3 349 1 OAS1_PIG	Q92592 sus scrofa
7	73.5	15.0 1260 1 LIN1_NYCCO	P038548 nycticebus
8	72	14.7 1953 1 CAR4_HUMAN	Q9y239 homo sapien
9	72	14.7 953 1 CAR4_MOUSE	Q8bib0 mus musculu
10	71	14.7 1087 1 OAS3_HUMAN	Q9ysk5 homo sapien
11	71	14.5 833 1 SYL_STRPN	Q97880 streptococc
12	70	14.3 192 1 OASB_MOUSE	Q61056 mus musculu
13	70	14.3 494 1 ENP2_CHICK	P79784 gallus galli
14	69.5	14.2 400 1 OAS1_HUMAN	P00973 homo sapien
15	69	14.1 833 1 SYL_STR6	Q8ibb6 streptococc
16	68	13.9 1034 1 BGAL_BACME	O52847 bacillus me
17	67.5	13.8 204 1 VNSC_PILHB	P32533 human parai
18	67.5	13.8 204 1 VNSC_PILHE	P32535 human parai
19	67.5	13.8 344 1 FLIG_BORBE	P52610 borreia bu
20	66.5	13.6 200 1 VIP_CHICK	P48143 gallus galli
21	66.5	13.6 468 1 SYE_THETH	P016939 caenorhabdi
22	66	13.5 455 1 ZPR1_CAEEL	P32532 human parai
23	66	13.5 804 1 SYL_STRAEL	P52610 borreia bu
24	66	13.5 807 1 SYL_STRPB	P48143 gallus galli
25	66	13.5 833 1 SYL_STRPB	P016939 caenorhabdi
26	65.5	13.4 322 1 YQJA_BACSU	P54538 bacillus su
27	65.5	13.4 430 1 ACDL_PIG	P79274 sus scrofa
28	65	13.4 1102 1 MYSC_CHICK	P29616 gallus galli
29	65	13.3 358 1 OAS1_RAT	Q05961 rattus norv
30	65	13.3 454 1 C5P2_MOUSE	Q5P2_MOUSE
31	65	13.3 454 1 PHK2_RHIME	Q922a4 rhizobium m
32	65	13.3 1242 1 NBNH_MOUSE	Q9q257 mus musculu
33	65	13.3 1242 1 NBNH_MOUSE	Q9q257 mus musculu
34	64	13.1 367 1 OSA_MOUSE	P11928 mus musculu
35	64	13.1 509 1 AURE_STRAU	P81177 staphylococc
36	64	13.1 833 1 SYL_STRAU	Q61645 mus musculu
37	64	13.1 1182 1 HAIK_MOUSE	P32534 human parai
38	63.5	13.0 204 1 VNSC_P11HD	P58801 mus musculu
39	63.5	13.0 539 1 RIK2_MOUSE	Q90660 gallus galli
40	63.5	13.0 611 1 BIR_CHICK	P27986 homo sapien
41	63.5	13.0 749 1 SPOT_SPICI	Q9TAH spiroplasma
42	63.5	13.0 1178 1 RPOB_TREPA	Q83269 treponema p
43	63.5	12.9 411 1 SVS_CAMEB	Q9pb1 campylobact
44	63	12.9 4466 1 DYC_ANTCR	P39057 anthocidari

for large proteins in vitro.";
 RN Res. 6:63-70(1999).
 [6] SEQUENCE OF 282-1473 FROM N.A. (ISOFORM 1).
 RC TISSUE=Uterus;
 RA Koehler K., Beyer A., Maves H.-W., Gassenshuber J., Wiemann S.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 CC FUNCTION: Able to form cytoplasmic structures termed death effector filaments. Enhances APAF1 and cytochrome c-dependent activation of pro-caspase-9 and consecutive apoptosis. Seems to bind ATP.
 CC -!- SUBUNIT: Interacts strongly with caspase 2, weakly with caspase 9 and with APAF1 in a cytochrome c-inducible way leading to the formation of an apoptosome. This interaction may be ATP-dependent.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=alternative splicing; Named isoforms=4;
 Name=1: Synonyms=NAC beta, DEFCAF-1;
 IsoId=Q9C00-1; Sequence=Displayd;
 Name=2: Synonyms=NAC alpha, DEFCAF-S;
 IsoId=Q9C00-2; Sequence=VSP_004327;
 Name=3: Synonyms=NAC gamma;
 IsoId=Q9C00-3; Sequence=VSP_004326, VSP_004327;
 Name=4: Synonyms=NAC delta;
 IsoId=Q9C00-4; Sequence=VSP_004326;
 CC -!- TISSUE SPECIFICITY: Widely expressed. Isoforms 1 and 2 are expressed in peripheral blood leukocytes, chronic myelogenous leukemia cellline K-562, followed by thymus, spleen and heart. Also detected in lung, placenta, small intestine, colon, kidney, liver and muscle.
 CC -!- SIMILARITY: Contains 1 DAPIN domain.
 CC -!- SIMILARITY: Contains 1 NACHT domain.
 CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.

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CC DR EMBL:AF288548; AACI5254_1;
 DR EMBL:AB310105; AAC30288_1;
 DR EMBL:AF229059; AAC00748_1;
 DR EMBL:AF229060; AAC00749_1;
 DR EMBL:AF229061; AAC00750_1;
 DR EMBL:AF229062; AAC00751_1;
 DR EMBL:AB03143; CAB5945_1;
 DR EMBL:AU117470; CAB5945_1;
 PIR: TI17255; TI1755;
 HSSP: PI3489; IAY4;
 MIM: 606636; -;

DR GO:GO:0005622; C:intracellular; IC.
 GO:GO:001650; F:Dopotosis activator activity; NAS.
 DR GO:GO:0008656; F:caspase activator activity; NAS.
 DR GO:GO:0019899; F:enzyme binding; IPI.
 DR GO:GO:0006919; P:caspase activation; NAS.
 InterPro: IPR001315; CARD.
 InterPro: IPR00067; Disease resist.
 InterPro: IPR001611; LRR.
 InterPro: IPR007091; LRR_RNinh.
 InterPro: IPR007111; NACT_NTPase.
 InterPro: IPR004020; PARD_DAPIN_dom.
 Pfam: PF00560; LRR_2.
 DR Pfam: PF05729; NACHT_1;
 DR PROSITE: PR00364; DISEASRS1ST.
 DR PROSITE: PS50209; CARD_1.
 DR PROSITE: PS50821; DAPIN_1.
 DR PROSITE: PS50837; NACHT_1.

KW Apoptosis; ATP-binding; Leucine-rich repeat; Repeat;
 KW Alternative splicing;
 FT DOMAIN 1 92
 FT DOMAIN 328 637
 FT REPEAT 704 725
 FT REPEAT 807 830
 FT REPEAT 864 887
 FT REPEAT 921 944
 FT REPEAT 950 973
 FT REPEAT 1199 1215
 FT REPEAT 1216 1236
 FT DOMAIN 1374 1463
 FT NP_BIND 334 341
 FT VARSPlic 958 987
 FT VARSPlic 1262 1305
 FT MUTAGEN 340 340
 FT MUTAGEN 340 340
 FT CONFLICT 155 155
 FT CONFLICT 246 246
 FT CONFLICT 782 782
 FT CONFLICT 878 878
 FT CONFLICT 995 995
 FT CONFLICT 1119 1119
 FT CONFLICT 1184 1184
 FT CONFLICT 1241 1241
 FT CONFLICT 1366 1366
 SQ SEQUENCE 1473 AA; 16565 MW; 438F0DCE45C2562D CRCG64;
 Query Match 100.0%; Score 490; DB 1; Length 1473;
 Best Local Similarity 100.0%; Pred. NO. 1.7e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFHFVDYREQLIARYTVEVYLDKLHGQVLSQEQYERVLAENTPSQMKLFSLSQSNDR 60
 DR 1379 LFHFVDYREQLIARYTVEVYLDKLHGQVLSQEQYERVLAENTPSQMKLFSLSQSNSWR 1438
 QY 61 KCKDGILQYALKETHPHLIMELWEKSSKKGLPLSS 95
 DR 1439 KCKDGILQYALKETHPHLIMELWEKSSKKGLPLSS 1473
 DE Apoptosis-associated speck-like protein containing a CARD (mASC)
 DE (PYCARD).
 GN ASC_mouse (Mouse).
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID:10030;
 STRAIN=BALB/C; TISSUE=Thymus;
 AC Q9E8B4; Q9D2W9;
 DT 16-OCT-2001 (Rel: 40, Created)
 DT 16-OCT-2001 (Rel: 40, Last sequence update)
 DT 10-OCT-2003 (Rel: 42, Last annotation update)
 DE Apoptosis-associated speck-like protein containing a CARD (mASC)
 DE (PYCARD).
 RN SEQUENCE FROM N.A.
 RN STRAIN=FVB/N; TISSUE=Breast tumor;
 RC Martinon F., Holmann K., Tschopp J.;
 RA "PyCard a PYD and CARD containing molecule.";
 RT "Murine ortholog of ASC, a CARD-containing protein, self-associates and exhibits restricted distribution in developing mouse embryos.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP

RC	STRAIN=C57BL/6J; TISSUE=Pancreas, and Tongue;	DR	EMBL; BC008252; AAH0825.1; -.	
RX	MEDLINE:21083660; PubMed:11217851;	DR	MGI; MGI:1931165; Asc.	
RA	Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y.,	DR	GO; GO:0005829; C-cytosol; IDA.	
RA	Aizawa K., Hara A., Fukunishi Y., Konno J., Adachi J., Fukuda S.,	DR	InterPro; IPR01315; CARD.	
RA	Aizawa K., Izawa M., Nishi K., Kiyoyswa H., Kondo S., Yamansaka I.,	DR	InterPro; IPR004020; PAPD_DAPIN_dcm.	
RA	Saito T., Okazaki Y., Gojobori T., Boni H., Kasukawa T., Saito R.,	DR	Pfam; PF02758; PAAD_DAPIN_1.	
RA	Kadota K., Matsuda H.A., Amburner M., Batalov S., Casavant T.,	DR	PROSITE; PS5009; CARD_1.	
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	DR	PROSITE; PS5024; DAPIN_1.	
RA	Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesce G., Quackenbush J.,	KW	Apoptosis; Anti-oncogene.	
RA	Schriml L.M.; Staudt P., Suzuki R., Tomita M., Wagner L., Washio T.,	FT	DAPIN.	
RA	Sakai K., Okido T., Furuno M., Aono H., Baldari R., Barsh G.,	DOMAIN	105 193 CARD	
RA	Blake J., Boeffel D., Boijunga N., Carninci P., de Bonaldo M.F.,	FT	CONFFLICT 159 159 K → E (IN REF. 3).	
RA	Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M.,	SQ	SEQUENCE 193 AA; 21458 MW; 2A4EA40194870B31 CRC64;	
RA	Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	Query Match	51.6%; Score 253; DB 1; Length 193;	
RA	Lyons P., Marchionni L., Mashima M.J., Mazzarelli J., Montaerts P.,	Best Local Similarity	61.2%; Pred. No. 4.6e-18;	
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,	Matches	49; Conservative 11; Mismatches 20; Indels 0; Gaps 0;	
RA	Sasaki H., Sato K., Schoenbach C., Soya T., Shibusawa Y., Stoch K.-P.,	QY	2 HFVDYREQLIARYTVEVYFLDKHGOVLSQEOYERVLAENTPSQMRLFSLSQSWDRK 61	
RA	Surumi H., Toyohoka K., Wang K.H., Whittaker C., Wilming L.,	Db	111 HFVDQRQALIARVTEVDGVLDALIGSVLTGQIQAVERETTSQDKMRKLFSFVPSWNL 170	
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,	QY	62 CKDGlyQALKETHPHIMEL 81	
RA	Hayashitaki Y.;	Db	171 CRDSEIQLALKETHPLVMDL 190	
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:655-690(2001).			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE:22388257; PubMed:12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	RESULT 3	ASC_HUMAN STANDARD; Q9HB00; Q9NKJ8;	
RA	Klausner R.D., Collins F.S., Wagner L., Schueler G.D., Schuler G.D.,	ID	Q9UEZ3; Q96D12; Q9BZ5; Q9HB00; Q9NKJ8;	
RA	Autschul S.F., Zeisberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,	AC	Q9UEZ3; Q96D12; Q9BZ5; Q9HB00; Q9NKJ8;	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	ID	Q9UEZ3; Q96D12; Q9BZ5; Q9HB00; Q9NKJ8;	
RA	Diatchenko L., Marusina K., Casavant T.L., Scheetz T.E.,	AC	Q9UEZ3; Q96D12; Q9BZ5; Q9HB00; Q9NKJ8;	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	DT	16-OCT-2001 (Rel. 40, Created)	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinchi P., Prange C.,	DT	16-OCT-2001 (Rel. 40, Last sequence update)	
RA	Raha S.A., Loqueland N.A., Peters G.J., Abramson R.D., Mulahy S.J.,	DT	16-OCT-2003 (Rel. 42, Last annotation update)	
RA	Bosak S.A., McEwan P.J., McCormick K.J., Malek J.A., Gunaratne P.H.,	DT	16-OCT-2003 (Rel. 42, Last annotation update)	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	DE	Apoptosis-associated speck-like protein containing a CARD (hASC)	
RA	Villanueva D.K., Muniz D.M.N., Sodergren E.J., Lu X., Gibbs R.R.,	DE	(PyCARD) (Target of methylation-induced silencing 1) (Caspase recruitment domain protein 5).	
RA	Fahy J., Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	DE	recruitment domain protein 5).	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	GN	ASC OR TMSL OR CARD\$.	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	OC	Homo sapiens (Human); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
RA	Schnarch A., Schein J.E., Jones J.M., Marra M.A.,	OX	NCBI_TaxID=9606;	
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";	RN	[1]_SEQUENCE FROM N.A. (ISOFORM 1).	
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RC	SEQUENCE FROM N.A. (ISOFORM 1).	
CC	-!- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic activity is mediated predominantly through the activation of caspase 9 (By similarity).	RC	MEDLINE=20036508; PubMed=10567338;	
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation, a redistribution from the cytoplasm to the aggregates occurs.	RC	MEDLINE=20035608; PubMed=10567338;	
CC	These appeared as hollow, perinuclear spherical, ball-like structures (By similarity).	RC	MEDLINE=20035608; PubMed=10567338;	
CC	-!- TISSUE SPECIFICITY: Expressed in small intestine, colon, thymus, spleen, brain, heart, skeletal muscle, kidney, lung and liver.	RC	MEDLINE=20552139; PubMed=11103776;	
CC	-!- DEVELOPMENTAL STAGE: Strongly expressed at E9.5 day in the telencephalon, thalamic areas of the diencephalon, heart and liver.	RC	MEDLINE=20552139; PubMed=11103776;	
CC	-!- SIMILARITY: Contains 1 DAPIN domain.	RC	MEDLINE=20552139; PubMed=11103776;	
CC	-!- SIMILARITY: Contains 1 CARD domain.	RC	MEDLINE=20552139; PubMed=11103776;	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RN	[3]_SEQUENCE FROM N.A. (ISOFORM 1).	
CC	DR	EMBL; AB032249; BAB16609.1;	RA	"CARD\$ protein is a CARD/PYRIN family member that is involved in apoptosis signal transduction.";
CC	DR	EMBL; AF310104; AA30287.1;	RT	"PyCard a PYD and CARD containing molecule.";
CC	DR	EMBL; AK009852; BAB26543.1;	RT	Submitted (SEP-2000) to the EMBL/GenBank/DBBJ databases.
CC	DR	EMBL; AK007742; BAB25229.1;	RL	[4] [5]
CC	DR	EMBL; AK018682; BAB31341.1;	RN	

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CC "CARDINAL, a novel caspase recruitment domain protein, is an inhibitor

CC of multiple NF-kappa B activation pathways.";

CC [6]

CC SEQUENCE FROM N.A. (ISOFORM SHORT) .

CC TISSUE=Kidney;

CC Guo J.H., Yu L.;

CC Submitted (MAY 2002) to the EMBL/GenBank/DDBJ databases.

CC [7]

CC CHARACTERIZATION, RT

CC MEDLINE=21402905; PubMed=11408476;

CC Pathan N., Marusawa H., Krajewska M., Matsuzawa S.-I., Kim H.,

CC Okada K., Toi I., Kitada S., Krajewski S., Welsh K., Pio F.,

CC Godzik A., Reed J.C.;

CC "TUCAN, an antiapoptotic caspase-associated recruitment domain family

CC protein overexpressed in cancer.";

CC J. Biol. Chem. 276:32220-32223(2001).

CC [8]

CC CHARACTERIZATION, AND MUTAGENESIS OF LEU-366.

CC MEDLINE=22062955; PubMed=12067710;

CC RX Pathan R., Leonardi A., Formisano L., Di Jess B., Vito P., Liguro D.;

CC RT "TUCAN/CARDINAL and DRAL participate in a common pathway for

CC modulation of NF-kappaB activation.";

CC PEBS Lett. 521:165-169 (2002).

CC [-] FUNCTION: Inhibits Nr-kappa-B activation. May participate in a

CC regulatory mechanism that coordinates cellular responses

CC controlled by NF-kappa-B transcription factor. Involved in the

CC negative regulation of caspase-1.

CC [-] SUBUNIT: May form homodimers. Interacts with FNBP3 (By

CC similarity).

CC [-] SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

CC [-] ALTERNATIVE PRODUCTS:

CC [-] Event=Alternative splicing; Named isoforms=2;

CC [-] Name=Short;

CC [-] Iso1=Q9Y2G2-1; Sequence=Displayed;

CC [-] CC

CC [-] TISSUE SPECIFICITY: High expression in lung, ovary, testis and

CC placenta. Lower expression in heart, kidney and liver. Also

CC expressed in spleen, lymph node and bone marrow.

CC [-] SIMILARITY: Contains 1 CARD domain

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CC or send an email to license@isb-sib.ch).

CC [9]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC MEDLINE=912446063; PubMed=10231032;

CC RA Nagae T., Isikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,

CC Miyajima N., Tanaka A., Kotani H., Ohara O.;

CC "Prediction of the coding sequences of unidentified human genes. XIII.

CC The complete sequences of 100 new cDNA clones from brain which code

CC for large proteins in vitro.";

CC RL J. Biol. Chem. 277:13952-13958 (2002).

CC [10]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC MEDLINE=2195061; PubMed=1181383;

CC RA Razmaria M., Srinivasula S.M., Wang L., Poyet J.-L., Geddes B.J.,

CC Di Stefano P.S., Bertin J., Ainemri E.S.;

CC RT "CARD-8 protein, a new CARD family member that regulates caspase-1

CC activation and apoptosis.";

CC RL J. Biol. Chem. 277:13952-13958 (2002).

CC [11]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RA Zhang H.;

CC "A novel apoptotic protein, NDPP1, containing CARD and BH3 domains.";

CC RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

CC [12]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RA Quiet C., Vito P.;

CC RT "DACA9, a novel CARD-containing protein.";

CC RT Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

CC [13]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RA

CC [14]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RA Quiet C., Vito P.;

CC RT "DACA9, a novel CARD-containing protein.";

CC RT Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

CC [15]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RP

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CC CHARACTERIZATION, RT

CC MEDLINE=21402905; PubMed=11408476;

CC Pathan N., Marusawa H., Krajewska M., Matsuzawa S.-I., Kim H.,

CC Okada K., Toi I., Kitada S., Krajewski S., Welsh K., Pio F.,

CC Godzik A., Reed J.C.;

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CC MEDLINE=22062955; PubMed=12067710;

CC RX Pathan R., Leonardi A., Formisano L., Di Jess B., Vito P., Liguro D.;

CC RT "TUCAN/CARDINAL and DRAL participate in a common pathway for

CC modulation of NF-kappaB activation.";

CC PEBS Lett. 521:165-169 (2002).

CC [-] FUNCTION: Inhibits Nr-kappa-B activation. May participate in a

CC regulatory mechanism that coordinates cellular responses

CC controlled by NF-kappa-B transcription factor. Involved in the

CC negative regulation of caspase-1.

CC [-] SUBUNIT: May form homodimers. Interacts with FNBP3 (By

CC similarity).

CC [-] SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

CC [-] ALTERNATIVE PRODUCTS:

CC [-] Event=Alternative splicing; Named isoforms=2;

CC [-] Name=Short;

CC [-] Iso1=Q9Y2G2-1; Sequence=Displayed;

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CC [-] TISSUE SPECIFICITY: High expression in lung, ovary, testis and

CC placenta. Lower expression in heart, kidney and liver. Also

CC expressed in spleen, lymph node and bone marrow.

CC [-] SIMILARITY: Contains 1 CARD domain

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CC [9]

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CC Miyajima N., Tanaka A., Kotani H., Ohara O.;

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CC RA Razmaria M., Srinivasula S.M., Wang L., Poyet J.-L., Geddes B.J.,

CC Di Stefano P.S., Bertin J., Ainemri E.S.;

CC RT "CARD-8 protein, a new CARD family member that regulates caspase-1

CC activation and apoptosis.";

CC RL J. Biol. Chem. 277:13952-13958 (2002).

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CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RA

CC [12]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

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CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RA Quiet C., Vito P.;

CC RT "DACA9, a novel CARD-containing protein.";

CC RT Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

CC [15]

CC SEQUENCE FROM N.A. (ISOFORM LONG) .

CC RP

FT	CONFLICT	422	L -> P (IN REF 5)		S -> R (IN REF 2).
SQ	SEQUENCE	431 AA;	48932 MW;	CBS4D10807732B6	CRC64;
Query Match	Score 19.3%; Best Local Similarity 32.5%; Matches 26;	Score 94.5%; Pred. No. 0.05%; Mismatches 17; Conservative	DB 1; Length 431; Indels 1; Gaps 1;		
Qy	3 FVDQYREQLIARTSVEVTLDKHL-GQVTSQEQQYERVLNENTRPSQMKLFSLSQSMDRK 61				
Db	347 FVKENHTRQARMGLDKGQDDQDNELTENKEVLEQEKTROSNEALLSNVEKKCDL 406				
Qy	62 CTDGLYQALKETPHPLIMEL 81				
Db	407 ALDVLFERSISERDPXLYVSYL 426				
RESULT 7					
	LIN1_NYCCO	STANDARD;	PRT;	1260 AA.	
	ID LIN1_NYCCO				
	AC P08548;				
	DT 01-AUG-1988 (Ref. 08, Last sequence update)				
	DE LINE-1 reverse transcriptase homolog.				
	OS Nycticebus coucang (Slow loris).				
	OC Mammalia; Eutheria; Primates; Strepsirrhini; Ioridae; Nycticebus.				
	OX NCBI_TaxID=5470;				
	RN [1]				
	RP SEQUENCE.				
	RX MEDLINE=86230917; PubMed=2423883;				
	RA Hattori M., Kuhara S., Takenaka O., Sakaki Y.;				
	RT "L1 family of repetitive DNA sequences in primates may be derived from a sequence encoding a reverse transcriptase-related protein";				
	RL Nature 321:625-628 (1986).				
	CC -1- MISCELLANEOUS: DETERMINED BY THESE AUTHORS BUT NOT SHOWN,				
	CC BELONGING TO THE LINE-1 FAMILY.				
	CC PIR; B5313; GNDL1.				
	DR HSSP; P2769; 1HD7.				
	DR InterPro; IPR05135; Exo_endo_phos.				
	DR InterPro; IPR00477; RVTS.				
	DR PF03312; Exo_endo_phos; 1.				
	DR Pfam; PF00078; rvt; 1.				
	KW RNA-directed DNA polymerase.				
	SQ SEQUENCE 1260 AA; 147042 MW; 7A6803DF471F7253 CRC64;				
Query Match	Score 15.0%; Best Local Similarity 23.0%; Matches 23;	Score 75%; Pred. No. 19; Conservative	DB 1; Length 1260;		
Qy	4 VDQYREQLIA---RVTISVEVVLDKHLGHQVLSQEQQYERVLNENTRPSQMRKLFSLSQWD 59				
Db	410 LNEYYKLYSHKYENLKEIDQYLEACHLPRLSQKEYVEML---NRPISSSETASTIONLP 465				
Qy	60 RIKCKDGG----LYQALKETPHPLIMELWEKGSKCCLP 92				
Db	466 KKSPGPDDGFTSEFYQTKEELVPLILNLQNIEKECILP 505				
RESULT 8					
	CAR4_HUMAN	STANDARD;	PRT;	953 AA.	
	ID CAR4_HUMAN				
	AC Q9Y339; Q81WFS5.				
	DT 28-FEB-2003 (Ref. 41, Created)				
	DE CASPase recruitment domain protein 4 (Nodl protein).				
	GN Homo sapiens (Human).				
	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	OC Mammalia; Eutheria; Primates; Strepsirrhini; Hominidae; Homo.				
	NCBI_TaxID=9606;				
	RN [1]				
	RP SEQUENCE FROM N.A.				
	RC TISSUE_Endothelial cells; PubMed=10224040;				
	RX MEDLINE=99240667; PubMed=10224040;				
CONFIRM	54	V -> F (IN REF 2)			

Berlin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R., Grant J.R., Keilty J.J., Goesselin M.L., Robison K.E., Wong G.H.W., Glucksmann M.A., Di Stefano P.S.; "Human CRD4 protein is a novel CED-4/Apaf-1 cell death family member that activates NF-kappaB." *J. Biol. Chem.* 274:12955-12958 (1999).

[2] RNP SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.
TISSUE=Breast;
RX-MEDLINE=99262599; PubMed=10329646;
RA-Inchiaro N., Roseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio R., Merino J., Liu D., Ni J., Nuñez G.; "Nod1, an Apaf-1-like activator of caspase-9 and nuclear factor-kappaB," *J. Biol. Chem.* 274:14560-14567(1999).

[3] RNP SEQUENCE FROM N.A.
TISSUE=Lymph;
RX-MEDLINE=22388257; PubMed=12477932;
RA-Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Raha S.S., Logue Llanio N.A., Peters G.J., Abramson R.D., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Keittman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.J., Schmutz J.J., Myers R.M., Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002).

[4] RNP FUNCTION=
RX-MEDLINE=21264704; PubMed=11058605;
RA-Inchiaro N., Ogura Y., Chen F.P., Moto A., Nuñez G.; RT-Human Nod1 confers responsiveness to bacterial lipopolysaccharides." *J. Biol. Chem.* 276:2551-2554 (2001).

-|- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-B activity via RICK (CARIIK, RIP2) and IKK-gamma. Confers responsiveness to intracellular bacterial lipopolysaccharides (LPS).
CC-SIMILARITY: Self-associates. Binds to Caspase-9 and RICK by CARD-CARD interaction.
CC-SUBCELLULAR LOCATION: Cytoplasmic.
CC-TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal muscle, pancreas, spleen and ovary. Also detected in placenta, lung, liver, thymus, testis, small intestine and colon.
CC-SIMILARITY: Contains 1 CARD domain.
CC-SIMILARITY: Contains 1 NACHT domain.
CC-SIMILARITY: Contains 9 leucine-rich (LRR) repeats.

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CC-EMBL: AF26484; AAD29125.1; DR-EMBL: AF149774; AAD43922.1; DR-EMBL: AF113925; AAD8350.1; DR-EMBL: BC040339; AAF40339.1; DR-Genew: HGNC:16390; CARD4. DR-MIM: 605980; -.

DR-GO: GO:0008656; P: caspase activator activity; TAS.
DR-GO: GO:0006915; P: apoptosis; TAS.
DR-InterPro: IPR001315; CARD.
DR-InterPro: IPR007091; LRR_RNain.
DR-InterPro: IPR007111; NACHT_NTPase.
DR-Pfam: PF00619; CARD_1.
DR-Pfam: PF05729; NACHT_1.
DR-PROSITE: PS50209; CARD_1.
DR-PROSITE: PS50837; NACHT_1.
KW-Repeat; Leucine-rich repeat.
FT-DOMAIN: CARD.
FT-DOMAIN: 15 105
FT-DOMAIN: 196 531
FT-NP_BIND: 202 209
FT-REPEAT: 632 656
FT-REPEAT: 702 725
FT-REPEAT: 727 750
FT-REPEAT: 755 778
FT-REPEAT: 783 806
FT-REPEAT: 819 862
FT-REPEAT: 867 891
FT-REPEAT: 895 918
FT-REPEAT: 923 946
FT-MUTAGEN: 41 41
FT-MUTAGEN: 783 806
FT-REPEAT: 839 862
FT-REPEAT: 867 891
FT-REPEAT: 895 918
FT-REPEAT: 923 946
V>Q; ABOLISHES CASPASE-9 ACTIVATION AND INTERACTION WITH RICK.
K>R; REDUCES CASPASE-9 ACTIVATION
R->H (IN REF 3).
CONFLICT: 447 447
SEQUENCE: 953 AA; 107690 MW; 0A9DF5FC648EB21A CRC64;
Query Match Score 72; DB 1; Length 953;
Best Local Similarity 14.7%; pred. No. 20;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;
Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
Match Score 72; DB 1; Length 953;
Best Local Similarity 29.1%; pred. No. 20;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;
Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
Match Score 72; DB 1; Length 953;
Best Local Similarity 29.1%; pred. No. 20;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;
Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
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Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
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Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
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Qy 8 REQLIARVTSEVVLDK-LHGQLSSEQYERVIAENTPSQMRKFLSOSWDRCKD-
Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
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Db 27 RELLYTHIRNFQCLVNLLKNDYFSAEADAIVCACTPDVKRLDLVQSKGBEVSEFF 86
Match Score 72; DB 1; Length 953;
Best Local Similarity 29.1%; pred. No. 20;

RA	Ravasi T., Reed D.J., Reid J., Ringwald M., Schneide C., Semple C.A., Setou M., Shimada K., Sandelin A., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Watanabe Y., Wells C., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,	FT	NP_BIND	202	209	ATP (POTENTIAL).
RA		FT	REPEAT	17	42	LRR 1.
RA		FT	REPEAT	702	725	LRR 2.
RA		FT	REPEAT	727	750	LRR 3.
RA		FT	REPEAT	755	778	LRR 4.
RA		FT	REPEAT	783	806	LRR 5.
RA		FT	REPEAT	839	862	LRR 6.
RA		FT	REPEAT	867	890	LRR 7.
RA		FT	REPEAT	895	918	LRR 8.
RA		FT	REPEAT	923	946	LRR 9.
RA		FT	REPEAT	984	984	S -> A (in strain Czech II).
RA	"Yasunori A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs.", Nature 420:563-573 (2002). [2]	SQ	SEQUENCE	953 AA;	107739 MW;	39G639621CBB158 CRC64;
RP	SEQUENCE FROM N.A. AND VARIANT ALA-884; STRAIN=Czech II, and FVB/N; TISSUE=Breast cancer; MEDLINE=12477932;	Query Match	Score 72;	DB 1;	Length 953;	
RC		Best Local Similarity	26.0%;	Pred. No. 20;		
RC		Matches 20;	Conservative	Mismatches 17;	Indels 2;	Gaps 2;
RC						
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schuler G.D., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Matsushina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bandal M.P., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.B., Schatz A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903 (2002).	QY	8 REQLIRVTSVEVILDK-LHQVLISCEOYRVLAAENTPSQMRLFSLSQSWDRKCKDGL 66			
RA		Db	27 REHHLVNTNQCLVNLLNGYFSQEDABIVCACTPKDVKRILDVQSKGEBVSBEFF 86			
RA		QY	67 YQALZETH-PHLIMEW 82			
RA		Db	87 LYVLQQLEDDATVDLRLW 103			
RA						
RA	RESULT 10 OR33_HUMAN ID_OAS3_HUMAN STANDARD; PRT;	RN				
RA	AC Q9Y6K5; Q9H3P5; DT 16-Oct-2001 (Rel. 40, Created) DT 10-Oct-2003 (Rel. 44, Last sequence update) DT 15-Mar-2004 (Rel. 43, Last annotation update)	RN				
RA	DE 2'-5'-oligoadenylate synthetase 3 (EC 2.7.7.-) ((2'-5') oligo(A) synthetase 3) (2'-5'A synthetase 3) (p100 QAS) (p100 QAS) (p100 QAS)	RN				
RA	DE DE GN OAS3. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	RN				
RA	RN [1] _ AND PARTIAL SEQUENCE. RN SEQUENCE FROM N.A. AND PARTIAL SEQUENCE. RN MEDLINE=99098839; PubMed=9880533;	RP				
RA	RA Rebonillat D., Hovnanian A., Marie I., Hovanessian A.G.; RA "The 100-kDa 2',5'-oligoadenylate synthetase catalyzing preferentially the synthesis of dimeric dpppA _n pS A molecules is composed of three homologous domains"; RA Perez L., Rasheed N.D., Renault B., Rowland K., Savage L., Scherer S.E., Shen H., Simon M., Stoval K., Timms K.M., Todd J., Itoh K.; RA RN [2] RN RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A. RN MEDLINE=21174977; PubMed=11280764;	RX				
RA	RA Ito M., Shichijo S., Tsuda N., Ochiai M., Harashima N., Saito N.,	RA				
CC	-- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD interaction (By similarity).	RA				
CC	-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	RA				
CC	-- SIMILARITY: Contains 1 CARD domain.	RT				
CC	-- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.	RT				
CC	-- CONTC: Contains 9 intracellular bacterial lipopolysaccharides (LPS) (By similarity).	RT				
CC	-- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD interaction (By similarity).	RT				
CC	-- SIMILARITY: Contains 1 CARD domain.	RT				
CC	-- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.	RT				
CC	-- CONTC: Contains 9 intracellular bacterial lipopolysaccharides (LPS) (By similarity).	RT				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. Its content is long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RT				
CC	DR EMBL; AK02663; BAC38566.1; -; DR EMBL; AK089662; BAC0940.1; -; DR EMBL; BC042670; AAH42670.1; -; DR EMBL; BC043670; AAH43670.1; -; MGI: MGI:1341839; Carda. InterPro; IPR001315; CARD. InterPro; IPR007091; LRR_RNinh. InterPro; IPR007111; NACT_NTPase. Pfam; PF00619; CARD_1. Pfam; PF05729; NACT_1. PROSITE; PS50269; CARD_1. PROSITE; PS50837; NACT_1. KW Apolosis; ATP-binding; Repeat; Leucine-rich repeat; Polymorphism. FT DOMAIN 15 107 CARD.	RA				
CC	FT DOMAIN 195 531 NACT.	RA				
CC	SEQUENCE OF 1-59 FROM N.A. RC TISSUE=Monocytes; MEDLINE=20564227; PubMed=1112351.	RP				

RA Rabouillet D., Hovanessian A., David G., Hovanessian A.G., Williams B.R.;
RT "Characterization of the gene encoding the 100-kDa form of human 2',
RT 5'-Oligoadenylate synthetase.";
RL Genomics 70:32-240 (2000).
RC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS
CC INFECTION; CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC OAS3 SYNTHESIZES PREFERENTIALLY DIMERIC 2',5'-OLIGOADENYLATE
CC MOLECULES. GTP CAN BE AN ALTERNATIVE SUBSTRATE.
CC -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
CC into PPP(A_nP_nA)_n oligomers, which activate the latent RNase L
CC that, when activated, cleaves single-stranded RNAs.
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: PRESENT AT HIGH LEVEL IN PLACENTA/TROPHOBlast.
CC -!- INDUCTION: BY Interferons.
CC -!- SIMILARITY: Belongs to the 2'-5A synthetase family.
CC
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or send an email to license@isb-sib.ch.)
CC
DR EMBL; AF063613; ADD2853.1; -.
DR EMBL; AB044545; BAB18647.1; -.
DR EMBL; PS000551; -; NOT_ANNOTATED_CDS.
DR EMBL; AF513515; -; NOT_ANNOTATED_CDS.
DR GenBank; HGNC:8088; OAS3.
DR MIN; 60351; -.
DR GO; GO:0005732; C:Microsome; TAS.
DR GO; GO:0006139; P:nucleobase; nucleoside, nucleotide and nucl.; TAS.
DR InterPro; IPR006117; 25A_SYNTH_2.
DR InterPro; IPR006116; 25A_SYNTH_2B.
DR InterPro; IPR002934; NTP_transf.
DR InterPro; IPR001201; PAP2'_core.
DR Pfam; PF01909; NTP_transf_2'_core.
DR PROSITE; PS000332; 25A_SYNTH_1.
DR PROSITE; PS008333; 25A_SYNTH_2.
DR PROSITE; PS5015; 25A_SYNTH_3.
KW RNA-binding; Transferase; Nucleotidyltransferase; Repeat.
KW Interferon induction.
FT DOMAIN 6 343 OAS DOMAIN 1.
FT DOMAIN 344 410 LINER.
FT DOMAIN 411 742 OAS DOMAIN 2.
FT DOMAIN 750 1084 OAS DOMAIN 3.
FT CONFLICT 18 18 R -> K (IN REF. 2).
FT CONFLICT 159 159 G -> A (IN REF. 1).
FT CONFLICT 249 249 A -> G (IN REF. 1).
FT CONFLICT 287 288 QL -> HV (IN REF. 1).
FT CONFLICT 316 316 L -> H (IN REF. 1).
FT CONFLICT 393 398 GAASIV -> AEPASY (IN REF. 1).
FT CONFLICT 503 504 HV -> QL (IN REF. 3).
FT CONFLICT 984 984 G -> R (IN REF. 2).
SQ SEQUENCE 1087 AA; 121164 MW; 3DABED08FF008ABA CRC64;

Query Match 14.7%; Score 72; DB 1; Length 1087;
Best Local Similarity 35.0%; Pred. No. 23;
Matches 21; Conservative 11; Mismatches 18; Indels 10; Gaps 4;

QY 42 NTRPQMRKFLFSLSWSW-DRKCKDGLYQALKETHPHL-TMEL-----WEKGSKKG 94
Db 193 NIRPAKLNLILLVHWHVQCLGLWW-KETLPPVYALELLTIFAMEQGCKKDAFSLA 249

RESULT 11
SYL_STRPN SYL_STRPN STANDARD; PRT; 833 AA.

AC Q97SS0; DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

QY 58 WDRKCKD---GLYQALKETHPHL-TMEL-----WEKGSKKG 89
Db 659 KFLDRYRLITSKELAENNGALDKYNEYVKAVTEQIES-LKFNTAIQLMVFNAAANK 717
Db 718 EDKLVVDYAKGPFIQQLIAPPAPHIAELWQTVATG 752

RESULT 12
OASB_MOUSE STANDARD; PRT; 192 AA.

AC Q60856; DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE 2'-5'-Oligoadenylate synthetase 1B (EC 2.7.7.-) ((2'-5')oligo(A)
DE synthetase 1b) (2'-5A synthetase 1B) (Fragment).
GN OAS1 OR OIAS2.
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
RN [1] RX SEQUENCE FROM N.A. MEDLINE=91232962; PubMed=1709495;
RX Rutherford M.N.; Kumar A.; Nissim A.; Chebath J.; Williams B.R.G./
RA "The murine 2'-5A synthetase locus: three distinct transcripts from two
RT linked genes.",
RT Nuclic Acids Res. 19:1917-1924 (1991).
RL :- FUNCTION: THE 2'-5A SYSTEM (THE OASS, 2'-5A, AND RNASE L) MAY PLAY A
CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL
GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC :- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + Phosphate.
CC :- COFACTOR: Requires calcium and magnesium.
CC :- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC :- PTM: Has probably disulfide bonds.
CC :- SIMILARITY: Belongs to the CD39 NTPase family.
CC

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or send an email to license@isb-sib.ch).

DR EMBL: X555982; CAA39455.1; -.
DR PIR: S15661; S15661.
DR MGD: MG19430; Oasib.
GO: GO:0003800; F:Antiviral response protein activity; IDA.
DR InterPro; IPR006117; 25A_Synth_2.
DR InterPro; IPR006116; 25A_Synth_2B.
DR PROSITE; PS0001201; PAP_25A_core.
DR PROSITE; PS000832; 25A_SYNTH_1; PARTIAL.
DR PROSITE; PS000833; 25A_SYNTH_2; PARTIAL.
DR RNA-binding; PS00152; 25A_SYNTH_3; 1.
KW Interferon induction.
FT NON_TER 1 192 AA; 21936 MW; 4E1C011EF9024F46 CRC64;
SQ SEQUENCE 192 AA; Score 70; DB 1; Length 192;
Query Match 14.3%; Pred. No. 5.4;
Best Local Similarity 33.3%; Mismatches 9; Indels 8; Gaps 2;
Matches 17; Conservative 9; Gaps 2;

QY 42 NTRPSMRKFLSLSQSWDRKCDGLYQALKETHPHLIMPL-----WEKGSK 87
137 NCRPKLRLRQLRVLVWYQCLKEKGDP-----QYQALULLTDAWEYGSR 184

RESULT 13
ID ENP2_CHICK STANDARD; PRT; 494 AA.
AC P79784;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ectonucleotide triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
DE (NTPase2) (Ecto-ATPase) (CD39 antigen-like 1).
GN ENTP2 OR CD39L1
OS Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
NCBI_TaxID=9031;
RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 68-73; 83-90; 108; 121;

RP 144-150; 154-176; 208-217; 251-258; 273-284; 337-352; 374-380;
RP RP 383-389; 448-456 AND 459-479.
RC TISSUE=Gizzard and Skeletal muscle;
RX MEDLINE=97150869; PubMed=8993405;
RA Kirley T.L.;
RT "Complementary DNA cloning and sequencing of the chicken muscle ecto-
ATPase. Homology with the lymphoid cell activation antigen CD39.";
RL J. Biol. Chem. 272:1076-1081(1997).
RN [2]
RN SEQUENCE OF 1-12 AND 154-176, AND CHARACTERIZATION.
RX MEDLINE=95081479; PubMed=7986647;
RA Stout J.G./Kirley T.L.;
RT "Purification and characterization of the ecto-Mg-ATPase of chicken
gizzard smooth muscle."
RL J. Biochem. Biophys. Methods 29:61-75(1994).
CC :- FUNCTION: In the nervous system, could hydrolyze ATP and other
nucleotides to regulate purinergic neurotransmission. Hydrolyzes
ADP only to a marginal extent (By similarity).
CC :- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + Phosphate.
CC :- COFACTOR: Requires calcium and magnesium.
CC :- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC :- PTM: Has probably disulfide bonds.
CC :- SIMILARITY: Belongs to the CD39 / CD39 NTPase family.
CC

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DR EMBL: U74467; AAC60071.1; -.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR PROSITE; PS01238; GDA1_CD39_NTPase; 1.
DR PROSITE; PF01150; GDA1_CD39_NTPase.
DR PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium.
FT INIT_MBT 0 0 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 3 POTENTIAL.
FT TRANSMEM 4 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 464 POTENTIAL.
FT TRANSMEM 465 485 POTENTIAL.
FT DOMAIN 486 494 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 8 13 POLY LEU.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 11 11 L->IL (IN REF. 2).
FT CONFLICT 174 176 L->IL (IN REF. 2).
SEQUENCE 494 AA; 54402 MW; 1E03E631DA61EE CRC64;
SQ Query Match 14.3%; Score 70; DB 1; Length 494;
Best Local Similarity 36.4%; Pred. No. 15; Mismatches 21; Indels 0; Gaps 0;

QY 21 VLDKLKGQVLQSQEQQYERVLAENTPSQMRKLFSLSQSWDRKCKD 64
Db 244 VLRKLSSKVLOAQENQETVANPCWPTGYRKLSLSRYSPCTE 287

RESULT 14
OAS1_HUMAN STANDARD; PRT; 400 AA.
ID OAS1_HUMAN ID OAS1_HUMAN
AC P00973; P04820; P29080; P78485; P78486; Q16700; Q16701;
AC Q96J51; AC Q96J51;
DT 21-JUL-1996 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 2'-5'-Oligoadenylate synthetase 1 (EC 2.7.-) ((2'-5')Oligo(A)
DE synthetase 1) (2'-5A synthetase 1) (P46/P42 OAS) (E18/B16).
GN OAS1 OR OIAS.
Homo sapiens (Human).

OS OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.
[1] RN SEQUENCE FROM N.A. (ISOFORM P41 AND P46).
RX MEDLINE=86081732; PubMed=2416561.
RA Benech P., Mory Y., Revel M., Chebath J.;
RT "Structure of two forms of the interferon-induced (2',-5') oligo(A) synthetase of human cells based on cDNAs and gene sequences.";
RL EMBO J. 4:2249-2256 (1985).
RN SEQUENCE FROM N.A. (ISOFORM P41).
RX MEDLINE=86222945; PubMed=3549863.
RA Shiojiri S., Fukunaga R., Ichii Y., Sokawa Y.;
RT "Structure and expression of a cloned cDNA for human (2',-5')oligoadenylate synthetase.";
RA Ruez G.A., Content J.;
RA Ruez G.A., Content J.;
RN "Full-length sequence and expression of the 42 kDa 2'-5A synthetase induced by human interferon.";
RT PERS Lett. 196:113-120 (1986).
RN SEQUENCE FROM N.A. (ISOFORMS P48 AND P41).
RX MEDLINE=8108911; PubMed=3153689;
RA Wathieu M.G., Moutschen S., Cavalier A., Dewit L., Defilippi P.,
Ruez G.A., Content J.;
RA Ghosh S.K., Kusari J., Bandhopadhyay S.K., Samanta H., Kumar R.,
Sen G.C.;
RT "Cloning, sequencing, and expression of two murine 2',-5'-oligoadenylate synthetases. Structure-function relationships.";
RL J. Biol. Chem. 266:15293-15299 (1991).
RN SEQUENCE FROM N.A.
RA Murzy D., Arenson A.D., Adams C., Burac C., Carvelli K., Chang J.,
Chacko J., Chen J., Ding Y., Dugan S., Durbin J., Forcum J.,
Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M.,
Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kovar C.,
Lau S., Leal B., Lee E., Li Y., Licharge O., Liu W., Logan O., Lu J.,
Ly T., Maroudi I., Martinez C., Merscher S., Montgomery K., Oswal G.,
Perez L., Rashid N.D., Renault B., Rowland K., Savage L., Sen G.C.,
Schreier S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J.,
Vo Q., Williamson A., Worley K.C., Yu W., Kucherlapati R., Nelson D.,
Gibbs R.A.;
RA Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN SEQUENCE FROM N.A. (ISOFORM P41).
RC TISSUE=Brain.
RX MEDLINE=22388557; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klaasner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Blat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang F., Hsieh F.,
Dianchenko L., Marcusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
Brown M.J., Urdin T.B., Toshiyuki Y., Carrinci P., Orange C.,
Raha S.S., Logueillo J., Abramson R.D., Mullally S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kertesman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shavachenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Kitzmiller M.T., Skalska U., Smilus D.E.,
Schnarch A., Schein J.B., Jones S.J.M., Marrs M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN SEQUENCE OF 255-364 FROM N.A. (ISOFORM P41).
RX MEDLINE=83273721; PubMed=6348777;

RA Merlin G., Chebath J., Benech P., Metz R., Revel M.;
RT "Molecular cloning and sequence of partial cDNA for
interferon-induced (2',-5')oligo(A) synthetase mRNA from human
cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 80:4904-4908 (1983).
RN [8]
RP SEQUENCE OF 221-400 FROM N.A. (ISOFORM P41), AND INDUCTION.
RT TISSUE=Lymphoblast;
RX MEDLINE=8528466; PubMed=2411547;
RA Saunders M.E., Gewirtz D.R., Tugwell M.E., McMahon M.,
Williams B.R.G.;
RT "Human 2'-A synthetase: characterization of a novel cDNA and
corresponding gene structure.";
RL EMBO J. 4:1761-1768 (1985).
RN SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=89082260; PubMed=31213131.
RA Watnelet M.G., Clauss T.M., Nols C.B., Content J., Ruez G.A.;
RT "New inducers revealed by the promoter sequence analysis of two
interferon-activated human genes.";
RL Eur. J. Biochem. 169:311-321 (1987).
RN SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88142842; PubMed=2830497;
RA Benech P., Vigneron M., Perez D., Revel M., Chebath J.;
RT "Interferon-responsive regulatory elements in the promoter of the
human 2',-5'-oligo(A) synthetase gene.";
RL Mol. Cell. Biol. 7:4498-4504 (1987).
RN SEQUENCE OF 1-27 FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=88283644; PubMed=2456211;
RA Rutherglen M.N., Hannigan G.E., Williams B.R.G.;
RT "Interferon-induced binding of nuclear factors to promoter elements
of the 2'-A synthetase gene.";
RL EMBO J. 7:751-759 (1988).
RN [11]
RP MUTAGENESIS OF CYS-331 AND LYS-333.
RX MEDLINE=990758; PubMed=9407111;
RA Ghosh A., Sarkar S.N., Guo W., Bachyopadhyay S., Sen G.C.;
RT "Enzymatic activity of 2',-5'-oligoadenylate synthetase is impaired by
specific mutations that affect oligomerization of the protein.";
RL J. Biol. Chem. 272:3220-3226 (1997).
RN SEQUENCE OF ASP-75 AND ASP-77.
RX MEDLINE=99395121; PubMed=1044285;
RA Sarkar S.N., Ghosh A., Wang H.W., Sung S.S., Sen G.C.;
RT "The nature of the catalytic domain of 2',-5'-oligoadenylate
synthetases.";
RL J. Biol. Chem. 274:25535-25542 (1999).
CC -1- FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS
CC -1- INFECTION; CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC -1- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
into PPP(A2'P5'A)n oligomers, which activate the latent RNase L.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH DIFFERENT SUBCELLULAR
CC -1- FRACTIONS SUCH AS MITOCHONDRIAL, NUCLEAR, AND ROUGH/SMOOTH
MICROSOMAL FRACTIONS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=p46; Synonyms=16 kDa, El18;
CC Isoid=Ph0973-1; Sequence=Displayed;
CC Name=p41; Synonyms=41 kDa, El16, 3-9;
CC Isoid=Ph0973-2; Sequence=VSP_003739;
CC Name=p48; Synonyms=9-2;
CC Isoid=Ph0973-3; Sequence=VSP_003740;
CC -1- INDUCTION: By interferons
CC -1- SIMILARITY: Belongs to the 2'-5A synthetase family
CC -1- CAUTION: Ref.8 sequence differs from that shown due to a
frame shift in position 400.
CC -1- CAUTION: Ref.4 sequence was originally thought to originate from

CC mouse but is a human sequence.

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DR EMBL; X02875; CAA26634_1;
 DR EMBL; X02874; CAA26633_1; -
 DR EMBL; M11809; AAB59552_1; -
 DR EMBL; M11805; AAB59552_1; JOINED.
 DR EMBL; M11806; AAB59552_1; JOINED.
 DR EMBL; M11807; AAB59552_1; JOINED.
 DR EMBL; M11808; AAB59552_1; JOINED.
 DR EMBL; M11810; AAB59553_1; -
 DR EMBL; D00068; BAA00047_1; -
 DR EMBL; X03371; CAB51602_1; -
 DR EMBL; M63850; AAA33885_1; ALT_INIT.
 DR EMBL; M63849; AAA33857_1; ALT_INIT.
 DR EMBL; BC0004551; - NOT_ANNOTATED_CDS.
 DR EMBL; BC000562; AAH00562_1; -
 DR EMBL; X02861; CAA26197_1; ALT_FRAME.
 DR EMBL; X06360; CAA2903_1; -
 DR EMBL; X027179; CAA31064_1; -
 DR EMBL; M18099; AAS59955_1; -
 DR EMBL; A14511; CAA01166_1; -
 DR EMBL; A14573; CAA01167_1; -
 PIR; A91013; SYH116.
 PIR; B24339; SYH118.
 Genew; HGNC:8086; OAS1.
 MIM; 164350.
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0006139; P: nucleobase, nucleoside, nucleotide and nucl. . . ; TAS.

DR Inter-Pro; IPR006117; 25A_SYNTH_2.
 DR Inter-Pro; IPR006116; 25A_SYNTH_UB.
 DR PROSITE; PS001201; PAP_25A_core.
 DR PROSITE; PS00832; 25A_SYNTH_I; 1.
 DR PROSITE; PS00833; 25A_SYNTH_2; 1.
 DR PROSITE; PS50152; 25A_SYNTH_3; 1.
 RNA-binding; Transcerase; Nucleotidyltransferase;
 KW Interferon induction; Alternative splicing.

Query Match Score 69 5; DB 1; Length 400;
 Best Local Similarity 32.0%; Pred. No. 14;
 Matches 16; Conservative 10; Mismatches 15; Indels 9; Gaps 2;

QY 44 RPSQMRKFLFSLQSQWDRKCDGlyQALKSTPHPHIMEL---WEKGSKK 88
 Db 201 RPTKLRSLTRVKHVNQCK---KKLGKPPQQVALELLTVAWERGSMK 246

RESULT 15

SYL STRR6 STANDARD; PRT; 833 AA.

ID Q8DB6; AC 10-Oct-2003 (Rel. 42, Created)
 DT 10-Oct-2003 (Rel. 42, Last sequence update)
 DT 10-Oct-2003 (Rel. 42, Last annotation update)
 DB Leucyl-tRNA synthetase (EC 6.1.1.4) (leucine--tRNA ligase) (LeuRS).
 GN LEUS OR SPR0215.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Strptococcus.
 OX NCBI_TaxID=171101;
 RN [1] -

RP SEQUENCE FROM N.A.
 RX MEDLINE=2142945; PubMed=11544234;
 RA Hoskins J.; Alborn W.E. Jr.; Arnold J.; Blaszczaik L.C.; Burgett S.;
 DeHoff B.S.; Estrem S.T.; Fritz L.; Fu D.-J.; Fuller W.; Geringer C.;
 Gilmour R.; Glass J.S.; Khoja H.; Kraft A.R.; Lagace R.E.,

RA LeBlanc D.J.; Lee L.N.; Lefkowitz E.J.; Lu J.; Matsushima P.;
 RA McAhren S.M.; McHenry M.; McNeaster K.; Mundy C.W.; Nicolas T.I.;
 RA Norris F.H.; O'Gara M.; Peery R.B.; Robertson G.T.; Rockey P.;
 RA Sun P.-M.; Winkler M.E.; Yang Y.; Young-Bellido M.; Zhao G.;
 RA Zook C.A.; Baltz R.H.; Jaskunas S.R.; Rostock P.R. Jr.; Skatrud P.L.,
 RA Glass J.I.;
 RT "Gene of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717 (2001).
 CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
 CC diiphosphate + L-leucyl-tRNA(Leu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC -1-
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 CC -1-
 CC DR EMBL; AE008404; AAK99039_1; -
 DR PIR; C97901; C97901; -
 DR HAMAP; MF_00049; -
 DR InterPro; IPR02300; Leu_tRNA_synt1a.
 DR InterPro; IPR01412; tRNA-synt_1a.
 DR InterPro; IPR09008; VALRS_11ERS_edit.
 DR Pfam; PF00133; tRNA-synt_1_1.
 DR PRINTS; PR00985; TRNASYNTHLEU.
 DR TIGRFAMS; TIGR00396; leus-bact; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE NEG_BACT; 1.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 DR KW Complete proteome.
 KW "HIGH" REGION.
 FT SITE 41 52
 FT SITE 610 614
 FT SITE 613 613 ATP (BY SIMILARITY)
 FT BINDING 613 613 "KMSKS" REGION.
 SO SEQUENCE 833 AA; 94366 MW; 53BA8C778AB19B9 CRC64;
 Query Match Score 69 1%; DB 1; Length 833;
 Best Local Similarity 25.3%; Pred. No. 34;
 Matches 24; Conservative 20; Mismatches 39; Indels 12; Gaps 4;
 KW
 QY 6 QYREQQLARYTSVEVY-----LDKLHGQVLIS--QEQQVERVIALENTRPSQMRKLFSLSS 57
 Db 659 KFLDRYLRLITSKETIAENNGALDGAAYNEVTAQMLVFNAAK 717
 QY 58 WDRKCKD-- GLYQALKETHPHLIMELWKGSKKG 89
 Db 718 EDKLYDYAGFCIAPPFAFLWQVVAETG 752

Search completed: July 28, 2004, 08:53:27
 Job time : 11.1566 secs

www-09-996-617-2_copy_1335_1429.rpr

Query Match 15.3%; Score 75; DB 2; Length 482;
 Best Local Similarity 24.1%; Pred. No. 8.8;
 Matches 21; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Db 466 RKKSPPPDGFTSEFQTFKEBLVILLNLFQNIEKEGILP 505

RESULT 5
 SYMSQ2
 15 VTSVEVLDKLHGQVLSQEQYERVLAENTRPSQRKLFSLQWDRKCKDGLYQALKETH 74
 (2'-5') oligo(A) synthetase (EC 2.7.7.-) 2 - mouse
 N; Alternative names: 2'-5'-oligoadenylate synthetase 2
 C; Species: Mus musculus (house mouse)
 C; Accession: A39417
 C; Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Sep-1998
 R; Ghosh, S. K.; Kusari, J.; Bandyopadhyay, S. K.; Samanta, H.; Kumar, R.; Sen, G. C.
 J. Biol. Chem. 266, 15289-15299, 1991
 A; Title: Cloning, sequencing and expression of two murine 2'-5'-oligoadenylate synthetase
 A; Reference number: A39417; PMID: 9132052; MUID: 9132052

Query Match 15.3%; Score 75; DB 1; Length 363;
 Best Local Similarity 25.3%; Pred. No. 9.9%;
 Matches 24; Indels 32; Gaps 4;

Db 22 LDKLKHQVLSSEQ YERVLAENTRPSQRKLFSLQW 58
 155 LDQLTQSYKPNPQIVRLIEBCTDQKEGFSTCFTELQDFLKQRPTRKPLKSLIRLVRHW 214

Query Match 14.9%; Score 73; DB 1;
 Best Local Similarity 25.3%; Pred. No. 9.9%;
 Matches 24; Indels 32; Gaps 4;

Db 59 DRKCKDGLYQALKETHPHLIMEL---WEKGSKK 88
 215 YQNCK---KRLGKLPQYALELLTVYAWERGSMK 245

RESULT 6
 C71005 hypothetical protein PH1337 - Pyrococcus horikoshii
 C; Species: Pyrococcus horikoshii
 C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
 C; Accession: C71005
 R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekiru, M.; Ohfuki, Y.; Furukashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon
 A; Reference number: A71000; MUID: 98344137; PMID: 967994
 A; Accession: C71005
 A; Cross-references: GB:AP000006; NID:G323633; PID:BA30431; PID:BA303386; PID:932577
 A; Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; GenBank accession number: A9381; MUID: 86230917; PMID: 2423883
 A; Gene: PH1337

Query Match 14.5%; Score 71; DB 2; Length 197;
 Best Local Similarity 22.5%; Pred. No. 7.7%;
 Matches 27; Indels 34; Gaps 5;

Db 2 HFVDQREQLIARYTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQRKLFSLQW 55
 21 HIAHESADMDTRIISMDABRAKURGEVYHQMDLILRERKGKHTAFDPYPTLPI 80

Query Match 15.0%; Score 73.5; DB 4; Length 1260;
 Best Local Similarity 23.0%; Pred. No. 38; Mismatches 38; Indels 15; Gaps 3;

Db 56 QSWDRKCD-----GLYQALKET-----PHPLIMEKGSKKGILP 94
 81 DIWEEERVKEARKSURLKVIAGTVGILAVTALLMVYTYPTIILGL-----GLPLA 133

RESULT 7
 410 LNEYKKLHSKYENLKEIDQYLEACHPLRLSQQEVEM----NRPISSSEIASTIONLP 465

Query Match 15.0%; Score 73; DB 1;
 Best Local Similarity 23.0%; Pred. No. 38; Mismatches 38; Indels 15; Gaps 3;

Db 4 VDQYREQOLIA---RVTSEVVLDKLHGQVLSQEQYERVLAENTRPSQRKLFSLQW 59

Query Match 14.5%; Score 71; DB 2; Length 197;
 Best Local Similarity 22.5%; Pred. No. 7.7%; Mismatches 21; Indels 34; Gaps 5;

Db 2 HFVDQREQLIARYTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQRKLFSLQW 55
 21 HIAHESADMDTRIISMDABRAKURGEVYHQMDLILRERKGKHTAFDPYPTLPI 80

Query Match 15.0%; Score 73.5; DB 4; Length 1260;
 Best Local Similarity 23.0%; Pred. No. 38; Mismatches 38; Indels 15; Gaps 3;

Db 56 QSWDRKCD-----GLYQALKET-----PHPLIMEKGSKKGILP 94
 81 DIWEEERVKEARKSURLKVIAGTVGILAVTALLMVYTYPTIILGL-----GLPLA 133

Query Match 14.5%; Score 71; DB 2; Length 197;
 Best Local Similarity 22.5%; Pred. No. 7.7%; Mismatches 21; Indels 34; Gaps 5;

Db 2 HFVDQREQLIARYTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQRKLFSLQW 55
 21 HIAHESADMDTRIISMDABRAKURGEVYHQMDLILRERKGKHTAFDPYPTLPI 80

Query Match 15.0%; Score 73.5; DB 4; Length 1260;
 Best Local Similarity 23.0%; Pred. No. 38; Mismatches 38; Indels 15; Gaps 3;

Db 56 QSWDRKCD-----GLYQALKET-----PHPLIMEKGSKKGILP 94
 81 DIWEEERVKEARKSURLKVIAGTVGILAVTALLMVYTYPTIILGL-----GLPLA 133

RESULT 7

RESULTS

H95029 leucine-tRNA synthetase [imported] - Streptococcus pneumoniae (strain TIGR4) C:Species: Streptococcus pneumoniae C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001 C:Accession: H95029 R:Tettelein, R.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heidorn, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Holtzapfel, Nson, T.; Hickey, E.K.; Holt, I.B. A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A:Reference number: A55000; MUID:21357209; PMID:11463916 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-833 <KUR> A:Cross-references: GB:AE005672; PIDN:AAK74433.1; PID:gi14971724; GSPDB:GN00164; TIGR:SP4 A:Experimental source: strain TIGR4 C:Superfamily: leucine-tRNA ligase C:Genetic code: SP0254 Query Match Score 71; DB 2; Length 833; Best Local Similarity 14.5%; Pred. No. 42; Matches 24; Conservative 21; Mismatches 38; Indels 12; Gaps 4; QY 6 CYREQLIARVTSVEV--LDKLHGSVLS-QEYERVLAENTRPSQNRKLFSLQS 57 Db 659 KFLDPRVRLTISKELAENGALDKVTETVKAVTEQIES-LKFNTAIQLMVFNANK 717 QY 58 WDRKCKD--GLNQALKETHPHLJMEWKGSKKG 89 Db 718 EDKLYVDVARGFIQIAPPAPHABELNCTVABTG 752

RESULT 8

S11561 (2'-5') oligo(A) synthetase (EC 2.7.7.-) Li - mouse (fragment) C:Species: Mus musculus (house mouse) C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999 C:Accession: S115661; S119108 R:Rutherford, M.N.; Kumar, A.; Niissim, A.; Chebath, J.; Williams, B.R.G. Nucleic Acids Res. 19, 1917-1924, 1991. A:Title: The murine 2'-5A synthetase locus: three distinct transcripts from two linked genes A:Reference number: S115660; MUID:91232962; PMID:1703495 A:Accession: S115661 A:Molecule type: mRNA A:Residues: 1-192 <RTU> A:Cross-references: EMBL:X559382 R:Williams, B. Submitted to the EMBL Data Library, September 1990 A:Reference number: S119108 A:Accession: S119108 A:Molecule type: mRNA A:Residues: 1-175, L', 177-192 <WIL> A:Cross-references: EMBL:X559382; PIDN:gi9714; PID:gi49715 C:Superfamily: Oligo(A) synthetase C:Keywords: nucleotidyltransferase

Query Match Score 70; DB 2; Length 192; Best Local Similarity 33.3%; Pred. No. 9.3; Matches 17; Conservative 9; Mismatches 17; Indels 8; Gaps 2;

RESULTS

SYH16 (2'-5') oligo(A) synthetase (EC 2.7.7.-), splice form E16 - human C:Species: Homo sapiens (man) C:Alternate name: Oligoadenylate synthetase C:Date: 14-Nov-1983 #sequence_revision 28-Dec-1987 #text_change 21-Jul-2000 C:Accession: A91013; JS0012; A23623; A01204; A24359 R:Benech, P.; Moty, Y.; Revel, M.; Chebath, J. EMBO J. 4, 2249-2256, 1985 C:Species: Mycoplasma pulmonis C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 22-Jun-2003

RESULTS

D90592 hypothetical protein MYPU_6440 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C:Species: Mycoplasma pulmonis C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 22-Jun-2003

RESULTS

QY 42 NTRPSQMRKLFSLSQWSWRICKDGLYQALKETHPHLIMEL----WEKGSK 87 Db 137 NCRCPTKIKLRLTRLYWQCLCKERLGDPLP--POYALELLTDWAEYGSR 184

RESULTS

SYH16 (2'-5') oligo(A) synthetase (EC 2.7.7.-), splice form E16 - human C:Species: Homo sapiens (man) C:Alternate name: Oligoadenylate synthetase C:Date: 14-Nov-1983 #sequence_revision 28-Dec-1987 #text_change 21-Jul-2000 C:Accession: A91013; JS0012; A23623; A01204; A24359 R:Benech, P.; Moty, Y.; Revel, M.; Chebath, J. EMBO J. 4, 2249-2256, 1985 C:Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of

A; Reference number: A91013; MUID:86081732; PMID:2416561
 A; Accession: A91013
 A; Molecule type: mRNA
 A; Residues: 1-364 <BEN>
 A; Cross-references: GB:K00006; NID:G35122; PIDN:CAA26633.1; PID:G35123
 R; Shiojiri, S.; Fukunaga, R.; Ichii, Y.; Sozawa, Y.
 J. Biochem. 99, 1455-1461, 1986
 A; Title: Structure and expression of a cloned cDNA for human (2'-5') oligoadenylate synthetase
 A; Reference number: A92003; MUID:86223945; PMID:3754863
 A; Accession: JJS0012
 A; Molecule type: mRNA
 A; Residues: 1-30, 'N', 32-114, 'P', 116-364 <SH>
 A; Cross-references: GB:D00668; GB:N00668; NID:9220080; PIDN:BA00047.1; PID:9220081
 R; Nathalet, M.; Moutschen, S.; Cravador, A.; Defilippi, P.; Huez, G.; Content, F.; Lett, 196, 113-120, 1986
 A; Title: Full-length sequence and expression of the 42 kDa 2'-5A synthetase induced by human
 A; Reference number: A23623; MUID:85108911; PMID:3753389
 A; Accession: A23623
 A; Molecule type: mRNA
 A; Residues: 1-10, 'N', 32-114, 'P', 116-294, 'T', 296-314, 'R', 316-364 <WAT>
 A; Cross-references: GB:X04371; GB:M2532; NID:G23792; PIDN:CA01602.1; PID:95650578
 C; Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA and
 C; Genetics: A; Gene: GDB:O1AS
 A; Cross-references: GDB:1119465; OMIM:164350
 A; Cross-position: 12pter-12qter
 C; Superfamily: Olig(A) synthetase
 C; Keywords: alternative splicing; nucleotidylyltransferase
 C; Molecule type: mRNA
 C; Species: Homo sapiens (man)
 C; Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 20-Apr-2000
 R; Benech, P.; Mory, Y.; Revel, M.; Chebath, J.
 EMBO J. 4, 2449-2516, 1985
 A; Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of human 2', 5'-oligonucleotides
 A; Reference number: A91013; MUID:86081732; PMID:2416561
 A; Accession: B24359
 A; Molecule type: mRNA
 A; Residues: 1-100 <BEN>
 A; Molecule type: DNA
 A; Residues: 2-78 <RES>
 A; Cross-references: GB:K00006; GB:X02875; NID:G189326; PIDN:AA59955.1; PID:G189326
 R; Benech, P.; Vigneron, M.; Peretz, D.; Revel, M.; Chebath, J.
 Mol Cell. Biol. 7, 4438-4504, 1987
 A; Title: Interferon-responsive regulatory elements in the promoter of the human 2', 5'-oligonucleotide synthetase
 A; Reference number: I57630; MUID:381142842; PMID:2830497
 A; Accession: I57630
 A; Status: translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 2-78 <RES>
 A; Cross-references: GB:K18099; NID:G189326; PIDN:AA59955.1; PID:G189326
 R; Nathalet, M.G.; Clauss, I.M.; Nols, C.B.; Content, J.; Huez, G.A.
 Eur. J. Biochem. 169, 313-321, 1987
 A; Title: New inducers revealed by the promoter sequence analysis of two interferon-activated genes
 A; Reference number: I37997; MUID:88082760; PMID:3121313
 A; Accession: I37997
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-28 <RE2>
 A; Cross-references: EMBL:X05560; NID:934393; PIDN:CAA29803.1; PID:G34394
 C; Comment: For alternate splice forms, see PIR:SYHUI6 and PIR:A22842.
 C; Comment: For alternate splice forms, see PIR:SYHUI6 and PIR:A22842.
 C; Genetics:
 A; Gene: GDB:O1AS
 A; Cross-references: GDB:119465; OMIM:164350
 A; Map position: 12pter-12qter
 C; Superfamily: Olig(A) synthetase
 C; Keywords: alternative splicing; nucleotidylyltransferase
 Query Match 14.2%; Score 69.5%; DB 1; Length 400;
 Best Local Similarity 32.0%; Pred. No. 25;
 Matches 16; Conservative 10; Mismatches 15; Indels 9; Gaps 2;
 Qy 44 RPSQMRKLFSLSQSWRKCDGLYQALKETHPHILMEL----WEKGSKK 88
 Db 201 RPTKLKSLRLVQHWNQNCK---KKLGKLUPOQYALELLTVYAWERGSMK 246
 RESULT 13
 SYMS03
 (2'-5') oligo(A) synthetase (EC 2.7.7.-) 3 - mouse
 N; Alternate names: 2'-5'-oligonucleotide synthetase 3
 C; Species: Mus musculus (house mouse)
 C; Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
 C; Accession: B39417
 R; Ghosh, S. K.; Kusari, J.; Bardwaj, S. K.; Samanta, H.; Kumar, R.; Sen, G.C.
 J. Biol. Chem. 266, 15293-15299, 1991
 A; Title: Cloning, sequencing, and expression of two murine 2'-5'-oligonucleotide synthetase genes
 A; Reference number: A39417; MUID:91332052; PMID:16151324
 A; Accession: B39417
 A; Molecule type: mRNA
 A; Residues: 1-14 <CHO>
 A; Cross-references: GB:M63850; NID:G200136; PIDN:AAA19858.1; PID:G200137
 A; Note: the authors translated the codon TRG for residue 259 as Arg
 C; Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA and
 C; Superfamily: Oligo(A) synthetase
 C; Keywords: nucleotidylyltransferase
 Query Match 14.2%; Score 69.5%; DB 1; Length 414;
 Best Local Similarity 32.0%; Pred. No. 26;
 Matches 16; Conservative 10; Mismatches 15; Indels 9; Gaps 2;
 Qy 44 RPSQMRKLFSLSQSWRKCDGLYQALKETHPHILMEL----WEKGSKK 88
 Db 201 RPTKLKSLRLVQHWNQNCK---KKLGKLUPOQYALELLTVYAWERGSMK 246
 RESULT 14
 A2842
 (2'-5') oligo(A) synthetase (EC 2.7.7.-), splice form 8-2 - human
 C; Species: Homo sapiens (man)
 C; Date: 20-Aug-1987 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
 C; Accession: A2842; M91013
 R; Saunders, M.E.J.; Gewert, D.R.; Tugwell, M.E.; McMahon, M.; Williams, B.R.G.
 EMBO J. 4, 1761-1768, 1985
 A; Title: Human 2'-5A synthetase: characterization of a novel cDNA and corresponding gene
 A; Reference number: A22842; MUID:85284966; PMID:2411547
 A; Accession: A22842
 A; Molecule type: mRNA
 A; Residues: 231-459 <SAU>
 A; Cross-references: GB:X02661; NID:G22795; PIDN:CAA26497.1; PID:G1335008
 A; Experimental source: interferon-induced Daudi lymphoblastoid cells
 R; Benach, P.; Mory, Y.; Revel, M.; Chebath, J.
 EMBO J. 4, 2249-2256, 1985
 A; Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of
 A; Reference number: A91013; MUID:86081732; PMID:2416561
 A; Accession: A91013
 A; Molecule type: mRNA
 A; Residues: 1-346 <BEN>
 A; Cross-references: GB:X02874; GB:K0006; NID:G15122; PIDN:CAA26633.1; PID:G15123
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 C; Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA and
 C; Comment: For alternate splice forms, see PIR:SYHUI8 and PIR:SYHUI6.

C:Genetics:

A:Gene: GDB:OIAS

A:Cross-references: GDB:119465; OMIM:164350

A:Map Position: 12pter-12qter

C:Superfamily: Oligo(A) synthetase

C:Keywords: alternative splicing; nucleotidyltransferase

Query Match 14.2%; Score 69.5; DB 2; Length 459;

Best Local Similarity 32.0%; Pred. No. 29;

Matches 16; Conservative 10; Mismatches 15; Indels 9; Gaps 2;

Qy 44 RPSGMRKPSLSSGSDRKKDGLYQALKETHPHILML---WERCSSK 88

Db 201 RPIKLKSILRLVIRKHWYQICK---KXKGKLPQQYALEBLTYAWERGSMK 246

RESULT 15

A43906 nuclear phosphoprotein xnf7 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 1-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000

C:Accession: A43906; S21947

R:Seddy, B.A.; Kloc, M.; Elkin, L.

Dev. Biol. 148, 107-116, 1991.

A:Title: The cloning and characterization of a maternally expressed novel zinc finger nu-

A:Reference number: A43906; MUID:92038424; PMID:1936552

A:Accession: A43906

A:Molecule type: mRNA

A:Residues: 1-609 <RED>

A:Cross-references: EML:1-609; PID:914915

A:Note: Sequence extracted from NCBI Backbone (NCBIN:64515, NCPIP:64520)

C:Genetics:

A:Gene: xnf7

C:Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology

C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger

F:141-190/Domain: RING finger homology <RNG>

Query Match 14.2%; Score 69.5; DB 2; Length 609;

Best Local Similarity 30.6%; Pred. No. 41;

Matches 26; Conservative 19; Mismatches 31; Indels 9; Gaps 4;

Qy 1 LHFDQYREGQLARTSVEVLDKRGQVLSQEQVERVAENRPSQRKRLFLSQSDR 60

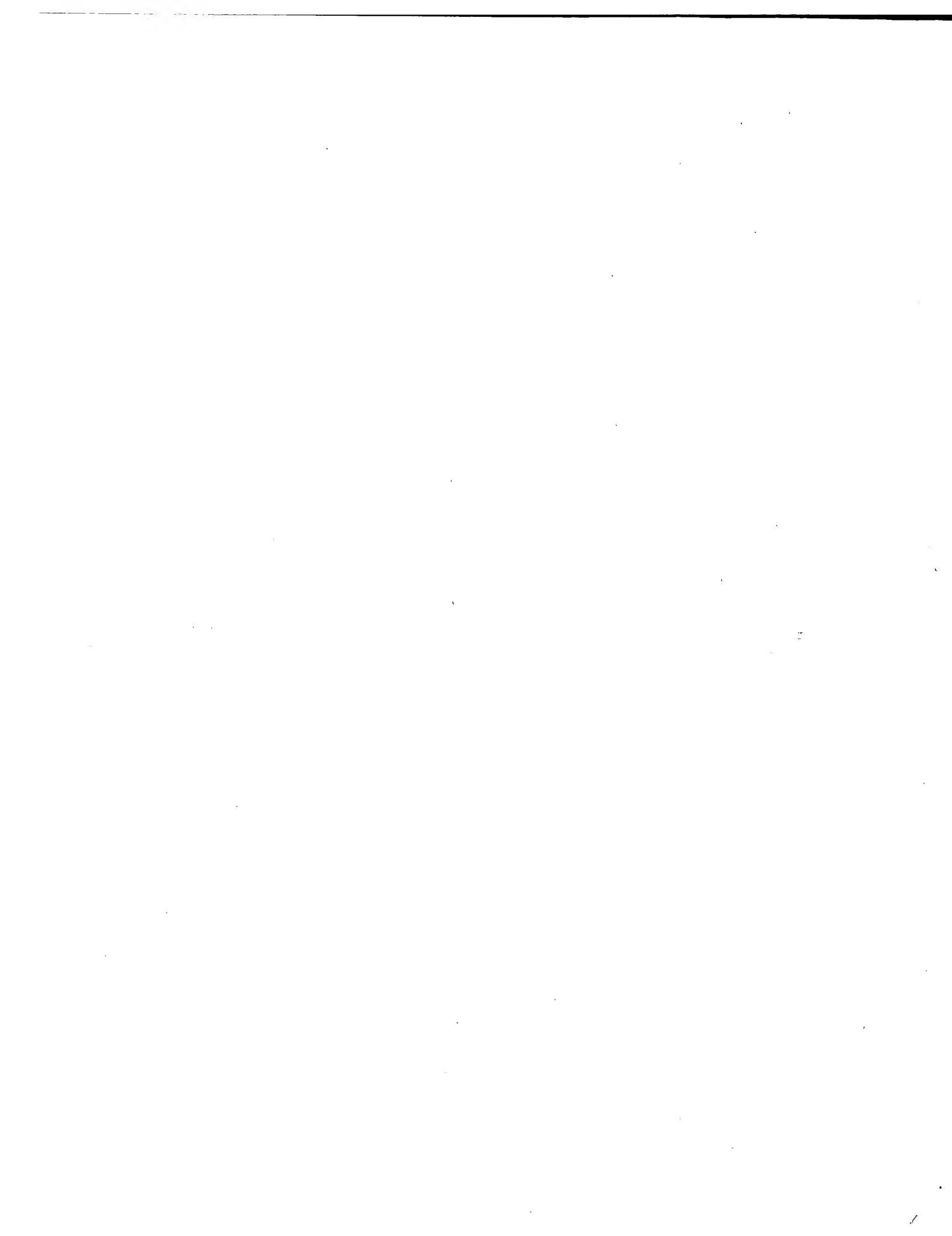
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Qy 61 XCKDGHLYQALKETHPHILMLWKG 85

Db 317 ----LHKFLDREERKLEQIKERQ 336

Search completed: July 28, 2004, 08:55:19

Job time : 15.7349 secs



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OM protein - Protein search, using sw model

Run on: July 28, 2004, 08:51:17 ; Search time 16:5964 Seconds
(without alignments)
295.514 Million Cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429

Perfect score: 490

Sequence: 1 LHFDQYREQLARVTSVEV.....HLMELWEGSKKKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Lassing First 45 summariesDatabase : Issued Patents AA-*
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3: /cgn2_6/prodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
1	253	51.6	193	4-US-09-340-620A-61	Sequence 61, Appl.
2	236	48.2	195	4-US-09-340-620A-49	Sequence 49, Appl.
3	216	44.1	71	4-US-09-340-620A-58	Sequence 58, Appl.
4	209	42.7	70	4-US-09-340-620A-57	Sequence 57, Appl.
5	209	42.7	70	4-US-09-340-620A-66	Sequence 66, Appl.
6	111.5	22.8	109	4-US-09-340-620A-71	Sequence 71, Appl.
7	72	14.7	164	4-US-09-245-281-41	Sequence 41, Appl.
8	72	14.7	164	4-US-09-207-359B-41	Sequence 41, Appl.
9	72	14.7	164	4-US-09-340-620A-41	Sequence 41, Appl.
10	72	14.7	164	4-US-09-340-620A-41	Sequence 41, Appl.
11	72	14.7	249	4-US-09-245-381-39	Sequence 39, Appl.
12	72	14.7	249	4-US-09-207-359B-39	Sequence 39, Appl.
13	72	14.7	249	4-US-09-340-620A-39	Sequence 39, Appl.
14	72	14.7	249	4-US-09-865-364-39	Sequence 39, Appl.
15	72	14.7	409	4-US-09-207-359B-46	Sequence 46, Appl.
16	72	14.7	409	4-US-09-865-364-41	Sequence 46, Appl.
17	72	14.7	953	4-US-09-099-41A-8	Sequence 8, Appl.
18	72	14.7	953	4-US-09-245-281-8	Sequence 8, Appl.
19	72	14.7	953	4-US-09-245-281-43	Sequence 43, Appl.
20	72	14.7	953	4-US-09-207-359B-8	Sequence 8, Appl.
21	72	14.7	953	4-US-09-207-359B-43	Sequence 43, Appl.
22	72	14.7	953	4-US-09-340-620A-8	Sequence 8, Appl.
23	72	14.7	953	4-US-09-340-620A-43	Sequence 8, Appl.
24	72	14.7	953	4-US-09-865-364-8	Sequence 8, Appl.
25	72	14.7	953	4-US-09-865-364-13	Sequence 43, Appl.
26	72	14.7	966	4-US-09-207-359B-47	Sequence 47, Appl.
27	72	14.7	966	4-US-09-865-364-47	Sequence 47, Appl.

RESULT 1
US-09-340-620A-61
; Sequence 61, Application US/09340620A.
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertan, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340-620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245-281
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/207-359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/093,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1999-02-06
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-61
Query Match 51.6%; Score: 253; DB: 4; Length: 193;
Best Local Similarity 61.2%; Pred. No. 3.5e-23;
Matches 49; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
QY 2 HFVDQYREQLARYTSEVYLTDKIHGQVISOEQYERVIAENTRPSQRKLPSLSQSQRDRK 61
Db 111 HFVDQYREQLARYTSEVYLTDKIHGQVISOEQYERVIAENTRPSQRKLPSLSQSQRDRK 61
; RESULT 2
US-09-340-620A-49
; Sequence 49, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertan, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340-620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245-281

PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207, 359
; CURRENT FILING DATE: 1998-12-08
; CURRENT APPLICATION NUMBER: US 09/340, 620A
; PRIOR FILING DATE: 1998-06-17
; CURRENT FILING DATE: 1999-06-28
; CURRENT APPLICATION NUMBER: US 09/245, 281
; PRIOR FILING DATE: 1999-02-05
; CURRENT FILING DATE: 1999-02-05
; CURRENT APPLICATION NUMBER: US 09/207, 359
; PRIOR FILING DATE: 1998-12-08
; CURRENT FILING DATE: 1999-02-06
; CURRENT APPLICATION NUMBER: US 09/099, 041
; PRIOR FILING DATE: 1998-06-17
; CURRENT FILING DATE: 1998-06-17
; CURRENT APPLICATION NUMBER: US 09/099, 041
; PRIOR FILING DATE: 1998-06-17
; CURRENT FILING DATE: 1998-06-17
; CURRENT APPLICATION NUMBER: US 09/019, 942
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 49
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-49

Query Match 48.2%; Score 236; DB 4; Length 195;
Best Local Similarity 56.8%; Pred. No. 4.3e-21;
Matches 46; Conservative 17; Mismatches 18; Indels 0; Gaps 0;
US-09-340-620A-57

Qy 1 LHFVDQYREQLIARTSVVLDKLGQVLSQEQYERVLAAENTPSOMKLFSLQSOSWDR 60
Db 112 LAFIDQRHAAILARTIVNVELLDALYKVLDEQYQAVRAEPTNSPKRKLFSFTPAWN 171

Qy 61 KCKDGLYQALKETHPHLIML 81
Db 172 TCKDLILQLARESQSYLVEDL 192

RESULT 3
US-09-340-620A-58
Sequence 58, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US 09/340, 620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245, 281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207, 359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099, 041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019, 942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-58

Query Match 44.1%; Score 216; DB 4; Length 71;
Best Local Similarity 61.4%; Pred. No. 3.2e-19;
Matches 43; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
US-09-340-620A-66

Qy 1 LHFVDQYREQLIARTSVVLDKLGQVLSQEQYERVLAAENTPSOMKLFSLQSOSWDR 60
Db 2 LHFIDQRHAAILARTIVNVELLDALYKVLDEQYQAVRAEPTNSPKRKLFSFTPAWN 61

Qy 61 KCKDGLYQAL 70
Db 62 TCKDLILQL 71

RESULT 4
US-09-340-620A-57
Sequence 57, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John

Qy 2 HFVDQYREQLIARTSVVLDKLGQVLSQEQYERVLAAENTPSOMKLFSLQSOSWDR 61
Db 2 HFVDQHQRHAAILARTIVNVELLDALYKVLDEQYQAVRAEPTNSPKRKLFSFTPAWNLT 61

Qy 62 CKDGLYQAL 70
Db 62 CKDSLQL 70

RESULT 5
US-09-340-620A-66
Sequence 66, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US 09/340, 620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245, 281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207, 359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099, 041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019, 942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 66

Query Match 42.7%; Score 209; DB 4; Length 70;
Best Local Similarity 60.9%; Pred. No. 2.3e-18;
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
US-09-340-620A-66

Qy 2 HFVDQYREQLIARTSVVLDKLGQVLSQEQYERVLAAENTPSOMKLFSLQSOSWDR 61
Db 2 HFVDQHQRHAAILARTIVNVELLDALYKVLDEQYQAVRAEPTNSPKRKLFSFTPAWNLT 61

Qy 62 CKDGLYQAL 70
Db 62 CKDSLQL 70

RESULT 6

US-09-340-620A-71
 Sequence 71; Application US/09340620A
 Patent No. 648233
 GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07334-124001
 CURRENT APPLICATION NUMBER: US/09/340, 620A
 PRIOR APPLICATION NUMBER: US 09/245, 281
 PRIOR FILING DATE: 1998-02-05
 PRIOR APPLICATION NUMBER: US 09/207, 359
 PRIOR FILING DATE: 1998-12-08
 PRIOR APPLICATION NUMBER: US 09/099, 041
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: US 09/019, 942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 71
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 71
 LENGTH: 109
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Consensus sequence
 NAME/KEY: VARIANT
 LOCATION: (1) ... (109)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-340-620A-71

Query Match 22.8%; Score 111.5; DB 4; Length 109;
 Best Local Similarity 42.0%; Pred. No. 3.6e-06;
 Matches 34; Conservative 15; Mismatches 25; Indels 7; Gaps 4;

Qy 4 VDQYREQIARVTS--VEVYDQLKHLGQ-VLSQYERYVLAENTRPSQRNLKPLSISQS-WD 59
 Db 11 IDQHXRALLIARVTEPXDSSIDALSRDLISEEDYEAETIXLSKVRKLILIVSRGE 70

Qy 60 RKCK--DGLYQALKETHPHL 77
 Db 71 ETCKXFLKCLQALKDSAAZL 91

RESULT 7
 US-09-245-281-41
 Sequence 41; Application US/09245281
 Patent No. 636916
 GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07334-1.18001
 CURRENT APPLICATION NUMBER: US/09/245, 281
 CURRENT FILING DATE: 1999-02-05
 EARLIER APPLICATION NUMBER: US 09/207, 359
 EARLIER FILING DATE: 1998-12-08
 EARLIER APPLICATION NUMBER: US 09/099, 041
 EARLIER FILING DATE: 1998-06-17
 EARLIER APPLICATION NUMBER: US 09/019, 942
 EARLIER FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 41
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-245-281-41

Query Match 14.7%; Score 72; DB 4; Length 164;
 Best Local Similarity 29.7%; Pred. No. 0.42;
 Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

Qy 27 RELVLTHIRNQCLVNLLNDYSAEDAETIVCACTQPDKVRKILDVSKGEEVESEFF 94
 Qy 65 -GLYQALKETHPHLIMELWEGSKKGLLPLS 94
 Db 87 LYLQQLADAYDLRPMLIEGSPSPSLTQS 117

RESULT 8
 US-09-207-359B-41
 Sequence 41; Application US/09207359B
 Patent No. 649140
 GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07334-112001
 CURRENT APPLICATION NUMBER: US/09/207, 359B
 CURRENT FILING DATE: 1998-12-08
 PRIOR APPLICATION NUMBER: US 09/099, 041
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: US 09/019, 942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 41
 LENGTH: 164
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-207-359B-41

Query Match 14.7%; Score 72; DB 4; Length 164;
 Best Local Similarity 29.7%; Pred. No. 0.42;
 Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

Qy 8 REQLIARVTSVEVLDK-LHGQVLSQYERYVLAENTRPSQRNLKPLSISQS-WD 64
 Db 27 RELVLTHIRNQCLVNLLNDYSAEDAETIVCACTQPDKVRKILDVSKGEEVESEFF 86

RESULT 9
 US-09-140-620A-41
 Sequence 41; Application US/09340620A
 Patent No. 6481933
 GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07334-124001
 CURRENT APPLICATION NUMBER: US/09/340, 620A
 CURRENT FILING DATE: 1999-06-28
 PRIOR APPLICATION NUMBER: US 09/245, 281
 PRIOR FILING DATE: 1999-02-05
 PRIOR APPLICATION NUMBER: US 09/207, 359
 PRIOR FILING DATE: 1998-12-08
 PRIOR APPLICATION NUMBER: US 09/099, 041
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: US 09/019, 942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 71
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 41
 LENGTH: 164
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-340-620A-41

Query Match 14.7%; Score 72; DB 4; Length 164;
 Best Local Similarity 29.7%; Pred. No. 0.42;
 Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

Qy 8 PROCTIARVTSVEVLDK-LHGQVLSQYERYVLAENTRPSQRNLKPLSISQS-WD 64

RESULT 10
US-09-865-364-41
 ; Sequence 41, Application US/09865364
 ; Patent No. 6613521
 GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 ; FILE REFERENCE: 07334-112001
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 09/207,359
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 09/099,041
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: US 09/019,942
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 41
 ; LENGTH: 164
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; SEQ ID NO: 39
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; SEQ ID NO: 39
 ; LENGTH: 249

Query Match 14.7%; Score 72; DB 4; Length 164;
 Best Local Similarity 29.7%; Pred. No. 0.42; Mismatches 14; Indels 4; Gaps 2;
 Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

Qy 8 REQLIARVTSVEVLDK-LHGQVLSSOEQYERVLAENTRPSQMRKLFSLSQSWSDRKCKD- 64
 Db 27 RELLVTHIRNTQCLVDNLKNDYFSAEADAEIVCACTQDKVRKILDLVQSKGEEVSFFP 86

Qy 65 -GLYQALKETHPHLIMELWEGSKKGLLPLS 94
 Db 87 LYLLQQIADAYVDLRPWLLEGFSPSLTQS 117

RESULT 11
US-09-245-281-39
 ; Sequence 39, Application US/09245281
 ; Patent No. 6369196
 GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
 ; FILE REFERENCE: 07334-112001
 ; CURRENT FILING DATE: 1999-06-28
 ; PRIOR APPLICATION NUMBER: US 09/245,281
 ; PRIOR FILING DATE: 1999-02-05
 ; PRIOR APPLICATION NUMBER: US 09/207,359
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 09/099,041
 ; PRIOR FILING DATE: 1998-06-17
 ; EARLIER APPLICATION NUMBER: US 09/019,942
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 39
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; SEQ ID NO: 39
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 14.7%; Score 72; DB 4; Length 249;
 Best Local Similarity 29.7%; Pred. No. 0.72; Mismatches 14; Indels 4; Gaps 2;
 Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

Qy 8 REQLIARVTSVEVLDK-LHGQVLSSOEQYERVLAENTRPSQMRKLFSLSQSWSDRKCKD- 64
 Db 27 RELLVTHIRNTQCLVDNLKNDYFSAEADAEIVCACTQDKVRKILDLVQSKGEEVSFFP 86

Qy 65 -GLYQALKETHPHLIMELWEGSKKGLLPLS 94
 Db 87 LYLLQQIADAYVDLRPWLLEGFSPSLTQS 117

RESULT 12
US-09-207-359B-39
 ; Sequence 39, Application US/09207359B
 ; Patent No. 6469140
 GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 ; FILE REFERENCE: 07334-112001
 ; CURRENT APPLICATION NUMBER: US/09/207,359B
 ; CURRENT FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 09/099,041
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: US 09/019,942
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 39
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; SEQ ID NO: 39
 ; LENGTH: 249

Query Match 14.7%; Score 72; DB 4; Length 249;
 Best Local Similarity 29.7%; Pred. No. 0.72; Mismatches 14; Indels 4; Gaps 2;
 Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

Qy 8 REQLIARVTSVEVLDK-LHGQVLSSOEQYERVLAENTRPSQMRKLFSLSQSWSDRKCKD- 64
 Db 27 RELLVTHIRNTQCLVDNLKNDYFSAEADAEIVCACTQDKVRKILDLVQSKGEEVSFFP 86

Qy 65 -GLYQALKETHPHLIMELWEGSKKGLLPLS 94
 Db 87 LYLLQQIADAYVDLRPWLLEGFSPSLTQS 117

RESULT 13
US-09-240-620A-39
 ; Sequence 39, Application US/09340620A
 ; Patent No. 6482933
 GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-124001
 ; CURRENT APPLICATION NUMBER: US/09/340,620A
 ; CURRENT FILING DATE: 1999-06-28
 ; PRIOR APPLICATION NUMBER: US 09/245,281
 ; PRIOR FILING DATE: 1999-02-05
 ; PRIOR APPLICATION NUMBER: US 09/207,359
 ; PRIOR FILING DATE: 1998-12-08
 ; EARLIER APPLICATION NUMBER: US 09/099,041
 ; EARLIER FILING DATE: 1998-06-17
 ; EARLIER APPLICATION NUMBER: US 09/019,942
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 39
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-340-620A-39

Query Match 14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72; Mismatches 4; Indels 4; Gaps 2;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARVTSVEVVLDK-LHGQVLSQLQEYERVLAENTPSQEMKLFSLSQSNDRKCD-- 64
Db 27 RELLVTHIRNTQCLVDNLRLNDYFSAEDAEIVCACTPQDFVKRILDLVQSKEEVSEFF 86

QY 65 -GLYQALKETPHLIMELWEGSKKGLPLS 94
Db 87 LYLLQQQJADAYVDLRPWLEIGFSPLSLTOS 117

RESULT 14
US-09-865-364-39
Sequence 39, Application US/09865364
Patent No. 6613521

GENERAL INFORMATION:
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865,364
PRIOR APPLICATION NUMBER: US/09/207,359
PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 39
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-865-364-39

Query Match 14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72; Mismatches 4; Indels 4; Gaps 2;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARVTSVEVVLDK-LHGQVLSQLQEYERVLAENTPSQEMKLFSLSQSNDRKCD-- 64
Db 27 RELLVTHIRNTQCLVDNLRLNDYFSAEDAEIVCACTPQDFVKRILDLVQSKEEVSEFF 86

QY 65 -GLYQALKETPHLIMELWEGSKKGLPLS 94
Db 87 LYLLQQQJADAYVDLRPWLEIGFSPLSLTOS 117

RESULT 15
US-09-207-359B-46
Sequence 46, Application US/09207359B
Patent No. 66169140

GENERAL INFORMATION:
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/207,359B
PRIOR APPLICATION NUMBER: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 46
LENGTH: 409
TYPE: PRT



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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:54:53 ; Search time 46.3554 Seconds

(without alignments)
 642.856 Million cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429
 Perfect score: 490
 Sequence: 1 LHFWQYREQLIARYTSEV.....HLIMELWEGSKKGLLPLSS 95

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published_Applications_AA.*

1: /cn2_6/ptodata/1/pupbaa/US07_PUBCOMB.pep:*

2: /cn2_6/ptodata/1/pupbaa/PCT_NEW_PUB.pep:*

3: /cn2_6/ptodata/1/pupbaa/US06_NEW_PUB.pep:*

4: /cn2_6/ptodata/1/pupbaa/US06_PUBCOMB.pep:*

5: /cn2_6/ptodata/1/pupbaa/US07_NEW_PUB.pep:*

6: /cn2_6/ptodata/1/pupbaa/PTCNS_PUBCOMB.pep:*

7: /cn2_6/ptodata/1/pupbaa/US08_NEW_PUB.pep:*

8: /cn2_6/ptodata/1/pupbaa/US08_PUBCOMB.pep:*

9: /cn2_6/ptodata/1/pupbaa/US09A_PUBCOMB.pep:*

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14: /gn2_6/ptodata/1/pupbaa/US10B_PUBCOMB.pep:*

15: /gn2_6/ptodata/1/pupbaa/US10C_PUBCOMB.pep:*

16: /gn2_6/ptodata/1/pupbaa/US10_NEW_PUB.pep:*

17: /gn2_6/ptodata/1/pupbaa/US60_NEW_PUB.pep:*

18: /gn2_6/ptodata/1/pupbaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	100.0	1399	9	US-09-388-221-4
2	490	100.0	1429	9	US-09-996-617-2
3	490	100.0	1429	9	US-09-931-071-2
4	490	100.0	1429	12	US-10-029-347-3
5	490	100.0	1429	12	US-10-029-347-26
6	490	100.0	1429	14	US-10-028-392-11
7	490	100.0	1429	14	US-10-028-374-3
8	490	100.0	1429	14	US-10-028-374-15
9	490	100.0	1429	14	US-10-183-770-3
10	490	100.0	1443	9	US-09-388-221-6
11	490	100.0	1473	9	US-09-388-221-2
12	490	100.0	1473	12	US-10-182-822-8
13	490	100.0	1473	12	US-10-182-822-8
14	427	87.1	88	9	US-09-841-739-15
15	427	87.1	88	14	US-10-449-315-15

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	100.0	1399	9	Sequence 4, Appli
2	490	100.0	1429	9	Sequence 2, Appli
3	490	100.0	1429	12	Sequence 3, Appli
4	490	100.0	1429	12	Sequence 26, Appli
5	490	100.0	1429	14	Sequence 11, Appli
6	490	100.0	1429	14	Sequence 3, Appli
7	490	100.0	1429	14	Sequence 15, Appli
8	490	100.0	1429	14	Sequence 3, Appli
9	490	100.0	1429	14	Sequence 15, Appli
10	490	100.0	1443	9	Sequence 15, Appli
11	490	100.0	1473	9	Sequence 8, Appli
12	490	100.0	1473	12	Sequence 8, Appli
13	490	100.0	1473	12	Sequence 15, Appli
14	427	87.1	88	9	Sequence 15, Appli
15	427	87.1	88	14	Sequence 15, Appli

Query Match Best Local Similarity 100.0%; Score 490; Length 1399;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1
 ; Sequence 4, Application US/09388221A
 ; Publication No. US20020192643A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; TITLE OF INVENTION: No. US20020192643A1 Card Proteins Involved in Cell Death Regul
 ; FILE REFERENCE: P-LJ 3650
 ; CURRENT APPLICATION NUMBER: US/09/388,221A
 ; CURRENT FILING DATE: 1999-09-01
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: Patentin ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 1399
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-388-221-4

Query Match Best Local Similarity 100.0%; Score 490; Length 1399;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHFVDQYEQLLARYTSVEVYLKDQVLSQEQYERVLAENTRPSQMRKLFSLSQSWSDR 60
 Db 1305 LHFVDQYEQLLARYTSVEVYLKDQVLSQEQYERVLAENTRPSQMRKLFSLSQSWSDR 1364
 Qy 61 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 95
 Db 1365 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 1399
 RESULT 2
 ; Sequence 2, Application US/09996617
 ; Patent No. US/002012819EA1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brittin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334 34 001
; CURRENT APPLICATION NUMBER: US/09/996,617
; CURRENT FILING DATE: 2001-11-27
; PRIORITY NUMBER: 09/931,071
; PRIORITY FILING DATE: 2001-08-15
; PRIORITY APPLICATION NUMBER: 09/428,252
; PRIORITY FILING DATE: 1999-10-27
; PRIORITY APPLICATION NUMBER: 09/340,620
; PRIORITY FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-996-617-2

Query Match 100.0% Score 490; DB 9; Length 1429;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Indels 0; Gaps 0;

Qy 1 LHFVDOYREQLIARYTSEVVLKDHGQVLSQEYERVLAENTPSQRKLFSLSQSQWDR 60
Db 1335 LHFVDOYREQLIARYTSEVVLKDHGQVLSQEYERVLAENTPSQRKLFSLSQSQWDR 1394

RESULT 3
US-09-931-071-2

; Sequence 2, Application US/09931071
; Patent No. US2002128219A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-335501
; CURRENT APPLICATION NUMBER: US/09/931,071
; CURRENT FILING DATE: 2002-03-18
; PRIORITY NUMBER: 09/428,252
; PRIORITY FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-931-071-2

Query Match 100.0% Score 490; DB 9; Length 1429;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Indels 0; Gaps 0;

Qy 1 LHFVDOYREQLIARYTSEVVLKDHGQVLSQEYERVLAENTPSQRKLFSLSQSQWDR 60
Db 1335 LHFVDOYREQLIARYTSEVVLKDHGQVLSQEYERVLAENTPSQRKLFSLSQSQWDR 1394

RESULT 4
US-10-029-347-3

; Sequence 3, Application US/10029347
; Publication No. US20030017562A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED

SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 11
 LENGTH: 1429
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-028-392-11

Query Match 100.0%; Score 490; DB 14; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 7.5e-46;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHFVDOYREQLIARTSVEVLDLKHGQVLSQEYERVLAENTRPSQRKLFSLSQSQWDR 60
 Db 1335 LHFVDOYREQLIARTSVEVLDLKHGQVLSQEYERVLAENTRPSQRKLFSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 95
 Db 1395 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 1429

RESULT 8
 US-10-028-374-15
 ; Sequence 15, Application US/10028374
 ; Publication No. US20030143706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
 ; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
 ; FILE REFERENCE: D0067A
 ; CURRENT APPLICATION NUMBER: US/10/183,770
 ; CURRENT FILING DATE: 2002-06-27
 ; PRIOR APPLICATION NUMBER: US 60/257,773
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 10/028,374
 ; PRIOR FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 15
 ; LENGTH: 1429
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-028-374-15

Query Match 100.0%; Score 490; DB 14; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 7.5e-46;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHFVDOYREQLIARTSVEVLDLKHGQVLSQEYERVLAENTRPSQRKLFSLSQSQWDR 60
 Db 1335 LHFVDOYREQLIARTSVEVLDLKHGQVLSQEYERVLAENTRPSQRKLFSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 95
 Db 1395 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 1429

RESULT 9
 US-10-183-770-3
 ; Sequence 3, Application US/10183770
 ; Publication No. US20030180812A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
 ; TITLE OF INVENTION: PREDOMINATELY IN BONE MARROW, HLRRBM1
 ; FILE REFERENCE: D0067A CIP
 ; CURRENT APPLICATION NUMBER: US/10/183,770
 ; CURRENT FILING DATE: 2002-06-27
 ; PRIOR APPLICATION NUMBER: US 60/257,773
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 10/028,374
 ; PRIOR FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 3
 ; LENGTH: 1429
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-183-770-3

Query Match 100.0%; Score 490; DB 14; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 7.5e-46;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHFVDOYREQLIARTSVEVLDLKHGQVLSQEYERVLAENTRPSQRKLFSLSQSQWDR 60
 Db 1335 LHFVDOYREQLIARTSVEVLDLKHGQVLSQEYERVLAENTRPSQRKLFSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 95
 Db 1395 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 1429

RESULT 10
 US-10-183-770-15
 ; Sequence 15, Application US/10183770
 ; Publication No. US20030180812A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: PREDOMINATELY IN BONE MARROW, HLRRBM1
 ; FILE REFERENCE: D0067A CIP
 ; CURRENT APPLICATION NUMBER: US/10/183,770
 ; CURRENT FILING DATE: 2002-06-27
 ; PRIOR APPLICATION NUMBER: US 60/257,773
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 10/028,374
 ; PRIOR FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 15
 ; LENGTH: 1429
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-183-770-15

QY 61 CKKDGLYQALKETHPHLIMELW 82
US-10-449-315-15
US-10-449-315-15
; Sequence 15, Application US/10449315
; Publication No. US20030190679A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,115
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US /09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US /09/691,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-15

Query Match 87.1%; Score 427; DB 14; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.8e-4;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTSVVFLDKLGQVLSQEQYERTAENTPSMRKLFSLSQEWDR 60
DB 7 LHFVDQYREQLIARTSVVFLDKLGQVLSQEQYERTAENTPSMRKLFSLSQEWDR 66

QY 61 CKKDGLYQALKETHPHLIMELW 82
Db 67 CKKDGLYQALKETHPHLIMELW 88

Search completed: July 28, 2004, 09:04:14
Job time : 47.3554 secs



PS Claim 15; Page 143-148; 184pp; English.

XX The present sequence is a human NB-ARC and CARD containing protein (NAC) isoform. NAC Gamma isoform represents the NAC splice variant in which both the splice regions are present in the translated polypeptide. NAC protein comprises a nucleotide binding (NB) domain (also referred as NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-Barrel-like domain. The caspases, cysteine aspartyl proteases, are principal effectors of apoptosis. CARD containing NAC proteins are used for screening modulators that modulates apoptosis, cytokine production, cytokine receptor signalling and other cellular processes. NAC can act as an immunogen for the production of monoclonal antibodies. It can also be used to diagnose and treat inflammatory disorders such as sepsis, fibrosis and arthritis and cancer pathologies such as adenocarcinomas and leukaemias

XX Sequence 1397 AA;

Query Match 100.0%; Score 490; DB 4; Length 1397;

Best Local Similarity 100.0%; Pred. No. 2.2e-48; Matches 95; Conservative 0; Nismatches 0; Indels 0; Gaps 0;

Qy 1 LHFVDOYREQUILARYTISVUVLDKLKGQVLSQEVYERVLAENTRSPQRKFLSLSQSMDR 60
Db 1303 LHFVDOYREQUILARYTISVUVLDKLKGQVLSQEVYERVLAENTRSPQRKFLSLSQSMDR 1362

Qy 61 KCKDGlyQALKETHPHLIMELWEKGSKKGHLPLSS 95
Db 1363 KCKDGlyQALKETHPHLIMELWEKGSKKGHLPLSS 1397

RESULT 2
AB6571 ID AAB62571 standard; protein; 1429 AA.
XX AC AAB62571,
XX DT 23-JUL-2001 (first entry)

XX Human CARD-7 polypeptide.

XX CARD-7; CARD-8; CARD-5; caspase recruitment domain; cancer; human; autoimmune disorder; antiinflammatory; immunosuppressive; antiallergic; antibacterial; antiviral; gene therapy.

XX OS Homo sapiens.

FH Key Location/Qualifiers
FT Domain 322..365 /note= "nucleotide binding domain"
FT Domain 333..341 /note= "kinase 1A subdomain"
FT Domain 404..413 /note= "motif 2 domain"
FT Domain 454..463 /note= "kinase 2 subdomain"
FT Domain 615..622 /note= "kinase 3a subdomain"
FT Domain 807..834 /note= "motif 2 domain"
FT Domain 836..863 /note= "leucine-rich domain"
FT Domain 864..891 /note= "leucine-rich domain"
FT Domain 893..920 /note= "leucine-rich domain"
FT Domain 921..948 /note= "leucine-rich domain"
FT Domain 950..976 /note= "leucine-rich domain"

XX PN WO200130813-A1.

PD 03-MAY-2001.
XX PP 27-OCT-2000; 2000WO-US029796.
XX PR 27-OCT-1999; 99US-00428252.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Bertin J;
XX DR WPI; 2001-243340/36.
XX PT Identifying a modulator of interaction between caspase recruitment domain (CARD)-7 and CARD-5, for treating autoimmune disorder, comprises measuring the binding of CARD-7 and CARD-5 in the presence of the compound.

XX SQ Disclosure; Fig 1A-D; 80pp; English.

XX CC The invention relates to identifying compounds, that modulate interaction between caspase recruitment domain (CARD)-7 and CARD-5. The method involves measuring the binding of CARD-7 and CARD-5 in the presence of the compound (an increase in the binding of CARD-7 to CARD-5 in the absence of the compound compared to the binding in the absence of the compound indicates that the compound is a modulator of CARD-7-CARD-5 interaction). Modulators of CARD-7 and CARD-8 expression or activity can be used to treat or diagnose disorders such as cancers, bacterial or viral infections, autoimmune disorders (systemic lupus erythematosus, immune-mediated glomerulonephritis or arthritis), inflammatory disorders, organ specific autoimmunity including multiple sclerosis, Hashimoto's thyroiditis, or Grave's disease, psoriasis, graft rejection, allergies. CARD-7 and CARD-8 are useful as modulating agents in regulating a variety of cellular processes including cell growth and cell death. The present sequence represents the human CARD-7, an intracellular protein

XX SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 4; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48; Matches 95; Conservative 0; Nismatches 0; Indels 0; Gaps 0;

Qy 1 LHFVDOYREQUILARYTISVUVLDKLKGQVLSQEVYERVLAENTRSPQRKFLSLSQSMDR 60
Db 1335 LHFVDOYREQUILARYTISVUVLDKLKGQVLSQEVYERVLAENTRSPQRKFLSLSQSMDR 1394

Qy 61 KCKDGlyQALKETHPHLIMELWEKGSKKGHLPLSS 95
Db 1395 KCKDGlyQALKETHPHLIMELWEKGSKKGHLPLSS 1429

RESULT 3
ABG7455 ID ABG7455 standard; protein; 1429 AA.
XX AC ABG7455;
XX DT 15-Nov-2002 (first entry)

XX DE Human caspase recruitment protein 7 protein.

XX XX Human; human leucine-rich repeat small intestine I; HLRRII; asthma; KW proliferative disorder; Gastrointestinal disorder; renal disorder; neural disorder; reproductive disorder; reproductive disorder; calcium regulation; apoptosis; immune system; anemia; human immune deficiency virus; HIV; cancer; blood coagulation disorder; autoimmune disorder; allergic reaction; inflammatory condition; cardiovascular disorder; ischaemia; neurological disorder; infection disease; cytokine production; expressed sequence tag; EST.

XX OS Homo sapiens.

XX PN WO200261086-A2.

XX PN WO200261086-A2.

KW	inflammatory condition; cardiovascular disorder; infectious disease; cytokine production;
KW	neurological disorder; ischaemia;
KW	expressed sequence tag; EST;
XX	Unidentified.
OS	XX
PN	XX
XX	WO200261086-A2.
XX	08-AUG-2002.
PD	08-AUG-2002.
XX	20-DEC-2001; 2000US-0257774P.
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	08-AUG-2002.
PD	20-DEC-2001; 2001WO-US049739.
PF	PR 22-DEC-2000; 2000US-0257774P.
XX	PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX	PI Feder J, Ramanathan C, Mintier G;
PT	PI Feder J, Ramanathan C, Mintier G;
PT	XX
PR	DR 2002-619252/66.
XX	WPI; 2002-619252/66.
PS	PR Disclosure; Page 229-233; 336pp; English.
XX	PT New isolated nucleic acid molecules encoding HLRSS1 polypeptides, or PT their fragments and homologues, useful for preventing, treating and PT ameliorating medical conditions, e.g. proliferative, gastrointestinal, or PT renal disorders.
CC	PT The invention relates to isolated nucleic acid molecules (I) encoding CC human leucine-rich repeat small intestine I (HLRSS1) polypeptides. The CC nucleic acid molecules and polypeptides are useful for preventing, CC treating and ameliorating medical conditions, such as proliferative, CC gastrointestinal, renal, neural, or reproductive disorders; or disorders CC related to aberrant calcium regulation or apoptosis modulation, either CC directly or indirectly. They are also useful for treating, preventing CC by activating or inhibiting the proliferation, differentiation, or CC mobilisation of immune cells; haematopoietic cells e.g. thrombocytopenia, CC anaemia; immunologic deficiency syndromes, e.g. human immune system virus (HIV) infection; HTLV-BLV infection; blood coagulation disorders, CC e.g. arterial thrombosis; autoimmune disorders, e.g. Addison's disease, CC myasthenia gravis; asthma or allergic reactions; inflammatory conditions, CC e.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer; CC cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias, CC aneurysms; neurological disorders, e.g. Alzheimer's disease, Huntington's CC chorea; infectious diseases e.g. measles, mumps, pneumonia, or viral, CC bacterial, and fungal infections. The HLRSS1 polypeptides are useful for CC modulating cytokine production, antigen presentation, or other processes CC such as boosting immune responses. ABC78454-ABG78474 represent HLRSS1 CC amino acid sequences and related amino acid sequences of the invention CC Sequence 1429 AA;
CC	Query Match 100.0%; Score 490; DB 5; Length 1429;
CC	Best Local Similarity 100.0%; Pred. No. 2.2e-48; Mismatches 0; Indels 0; Gaps 0;
CC	Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	Sequence 1429 AA;
CC	Query Match 100.0%; Score 490; DB 5; Length 1429;
CC	Best Local Similarity 100.0%; Pred. No. 2.2e-48; Mismatches 0; Indels 0; Gaps 0;
CC	Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	Sequence 1429 AA;
QY	1 LHFVDQYREQLIARVTSVEVLDLKGQVLSQEYERVLAENTRPSQRKLFSLSQSMDR 60
Db	1335 LHFVDQYREQLIARVTSVEVLDLKGQVLSQEYERVLAENTRPSQRKLFSLSQSMDR 1394
QY	1 LHFVDQYREQLIARVTSVEVLDLKGQVLSQEYERVLAENTRPSQRKLFSLSQSMDR 60
Db	1395 KCKDGLYQALKETHPHLIMELWEKGSKKGLPLSS 95
QY	61 KCKDGLYQALKETHPHLIMELWEKGSKKGLPLSS 95
Db	1395 KCKDGLYQALKETHPHLIMELWEKGSKKGLPLSS 1429
RESULT 5	Leucine-rich repeat (LRR) domain containing protein #2.
ABB7916	Human; human leucine-rich repeat small intestine I; HLRSS1; asthma; proliferative disorder; gastrointestinal disorder; renal disorder; neural disorder; calcium regulation; apoptosis; immune system; anaemia; human immune deficiency virus; HIV; cancer; blood coagulation disorder; autoimmune disorder; allergic reaction;
ID	ABB7916 standard; protein; 1429 AA.
XX	
AC	
XX	
DB	1335 LHFVDQYREQLIARVTSVEVLDLKGQVLSQEYERVLAENTRPSQRKLFSLSQSMDR 1394
QY	61 KCKDGLYQALKETHPHLIMELWEKGSKKGLPLSS 95
Db	1395 KCKDGLYQALKETHPHLIMELWEKGSKKGLPLSS 1429
15-NOV-2002 (first entry)	
ABG78472	Leucine-rich repeat (LRR) domain containing protein #2.
ABG78472	Human; human leucine-rich repeat small intestine I; HLRSS1; asthma; proliferative disorder; gastrointestinal disorder; renal disorder; neural disorder; calcium regulation; apoptosis; immune system; anaemia; human immune deficiency virus; HIV; cancer; blood coagulation disorder; autoimmune disorder; allergic reaction;
AC	
XX	
DT	07-OCT-2002 (first entry)

DE Human leucine-rich repeat domain containing protein KIAA0026.
 XX Human; leucine-rich repeat; HLRBM1; proliferative disorder;
 immune condition; apoptosis; signal transduction; autoimmune disease;
 haemopoietic cell disease; graft-versus-host disease; allergy; asthma;
 KW cardiovacular disorder; neurological disease; bierone;
 KW pulmonary disease; chronic obstructive pulmonary disease;
 allergic rhinitis; bronchial hyperresponsiveness; reproductive disease;
 haemopoietic disease; platelet disorder; systemic lupus erythematosus;
 KW cardiovascular disorder; systemic lupus erythematosus;
 KW cancer; KIAA0026.
 XX Homo sapiens.
 XX WO200252011-A2.
 XX PD 04-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-US049740.
 XX PR 22-DEC-2000; 2000US-0257773P.
 XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Feder J., Ramanathan C., Mintier G.;
 XX DR WPI; 2002-5666676/60.
 XX PT New HLRBM1 nucleic acids for preventing, treating or ameliorating e.g.
 proliferative disorders, immune conditions, a disorder related to
 aberrant apoptosis modulation or developmental disorders.
 XX PS Example 1; Page 362-366; 371pp; English.
 XX CC The present sequence represents a human leucine-rich repeat domain
 containing protein, which was used to search for leucine-rich
 repeat containing protein HLRBM1. HLRBM1 polypeptides and
 polynucleotides are useful for preventing, treating or ameliorating a
 medical condition such as a proliferative disorder, immune condition, or
 a disorder related to aberrant apoptosis modulation, either directly or
 indirectly, and in modulating signal transduction activity in various
 cells, tissue and organisms. They are also useful for treating,
 preventing, or diagnosing diseases of haematopoietic cells, autoimmune
 disease, graft-versus-host disease, allergic conditions (e.g. asthma),
 cardiovascular disorders, and neurological diseases, and for increasing
 the organisms' ability to synthesize and/or release pheromones. The
 polypeptide may also be used in treating, preventing or ameliorating
 pulmonary disease (e.g. chronic obstructive pulmonary disease, allergic
 rhinitis or bronchial hyperresponsiveness), reproductive disease,
 haemopoietic disease, platelet disorders (e.g. Bernard-Soulier
 syndrome), non-infectious disorders (e.g. innate immunity to bacterial
 pathogens, or adaptive immune response), immune and inflammatory
 disorders (e.g. systemic lupus erythematosus), cardiovascular diseases
 and cancers. HLRBM1 nucleic acids may further be used in chromosome
 identification or mapping, as a chromosome marker, as molecular weight
 markers, as diagnostic probes, in gene therapy, in raising anti-DNA
 antibodies, or as antigens for eliciting immune responses
 XX Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 5; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 2,2e-48;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ Sequence 1429 AA;

Qy 1 LHFVQREQLIARTVSVPEVVLQDKLHGQVLSQEQYERLAENTRPSQMRKLFSLSQWDR 60
 Db 1335 LHFVQREQLIARTVSVPEVVLQDKLHGQVLSQEQYERLAENTRPSQMRKLFSLSQWDR 1394

Qy 61 KCRDGLYQALKETHPHLMELWKGSKKCLPLSS 95
 Db 1395 KCRDGLYQALKETHPHLMELWKGSKKCLPLSS 1429

Qy 1 LHFVQREQLIARTVSVPEVVLQDKLHGQVLSQEQYERLAENTRPSQMRKLFSLSQWDR 60
 Db 1335 LHFVQREQLIARTVSVPEVVLQDKLHGQVLSQEQYERLAENTRPSQMRKLFSLSQWDR 1394

Qy 61 KCRDGLYQALKETHPHLMELWKGSKKCLPLSS 95

Db 1395 KCKDGLYQALKETHPHLIMELWKGSKGLPLSS 1429

RESULT 7

AA017855 standard; protein; 1429 AA.

XX

AC

XX

DT 20-AUG-2002 (first entry)

Pyrin domain containing protein NALP1-hs.

XX

Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian; antiarteriosclerotic; antiapoptotic; antibacterial; virucide; neuroprotective; antiarthritic; antirheumatic; antisthmatic; nephrotropic; osteoprotective; nootropic; intracellular signal transduction; inflammation; Alzheimer's disease; infection; Psoriasis; asthma; arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis; osteoarthritis; glomerulonephritis.

XX

Unidentified.

OS

PN

WO200240668-A2.

XX

PD

23-MAY-2002.

XX

PP

30-OCT-2001; 2001WO-EP012545.

XX

PR

15-NOV-2000; 2000DE-01056687.

XX

PA

(APOT-) APOTECH RES & DEV LTD.

XX

PI

Tschopp J, Martinon F;

XX

DR

WPI; 2002-427093/45.

XX

N-PSDB; AAI47127.

XX

New DNA encoding protein with pyrin domain, useful for treating diseases

PT involving impaired signal transduction, particularly inflammation, also

PT proteins and antibodies.

XX

PS

Claim 5; Fig 1; 116pp; German.

XX

The present invention relates the DNA and their encoded proteins, where the proteins contain at least one PYD (pyrin) domain. These can be used to treat diseases associated with impaired intracellular signal

CC arteriosclerosis, bacterial or viral infections (particularly meningitis CC and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma, CC sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's CC and Parkinson's diseases. The present sequence is a protein of the CC invention

XX

SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 5; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Mismatches 0; Indels 0; Gaps 0;

Matches 95; Conservative 0;

1 LHFVDQREQLIARTSVEVILKQVLSQEVRLVNTRSPQMRKLFLSOSMQR 60

Db 1335 LHFVDQREQLIARTSVEVILKQVLSQEVRLVNTRSPQMRKLFLSOSMQR 1394

OY 61 KCKDGLYQALKETHPHLIMELWKGSKGLPLSS 95

Db 1395 KCKDGLYQALKETHPHLIMELWKGSKGLPLSS 1429

RESULT 8
ABG71631

ID ABC71631 standard; protein; 1429 AA.

XX

AC

XX

DT 09-JAN-2003 (first entry)

XX Human caspase recruitment domain-7 (CARD-7).

XX Human; caspase activity; caspase recruitment domain-7; CARD-7; caspase-1;

XX ABG71631;

XX

Human caspase recruitment domain-7 (CARD-7).

XX Human; caspase activity; caspase recruiting enzyme; IL-1beta; pseudoICE;

XX ICEBERG; cell growth; cell death; inflammation; apoptosis;

XX caspase activation; cancer; Follicular lymphoma; leukemia; melanoma;

XX colon cancer; lung carcinoma; viral infection; autoimmune disease;

XX systemic lupus erythematosus; reactive arthritis; ALS;

XX human immunodeficiency virus infection; HIV infection;

XX Alzheimer's disease; Parkinson's disease; azytolytic lateral sclerosis;

XX myocardial infarction; stroke; inflammatory disorder; Crohn's disease;

XX insulin dependent diabetes mellitus; multiple sclerosis; psoriasis;

XX graft rejection; allergic rhinitis; food allergy; conjunctivitis;

XX glomerular nephritis; cytosolic; virucide; immunosuppressive;

XX dermatological; nephrotropic; neuroprotective; cardiant.

XX Homo sapiens.

OS

XX US2002128219-A1.

XX PN

US200240668-A2.

XX PD

12-SEP-2002.

XX PP

2001JUS-00931071.

XX PR

15-AUG-2001; 99US-00428252.

XX PR

27-OCT-1999; 99US-00428252.

XX PA

(BERT/) BERTIN J.

PA (ALNE/) ALNEMRI E S.

XX PI

Bertin J, Alnemri ES;

XX XX WPI; 2003-028968/02.

DR N-PSDB; ABSS5497.

XX

Assays for identifying compound that modulates the interaction of caspase

PT recruitment domain-8 with a CARD-8 ligand or a compound that modulates

PT activity of CARD-8.

XX Disclosure; Fig 1; 49pp; English.

XX

The present invention relates to methods of identifying compounds that regulate caspase activity using caspase recruitment domain-7 (CARD-7) or caspase recruitment domain-8 (CARD-8). In particular, a method for identifying a compound that modulates the interaction between CARD-8 and caspase-1, pseudo-interleukin-1 (IL-1) beta converting enzyme (pseudoICE) or ICEBERG is disclosed. CARD-7 and CARD-8 molecules are useful as modulating agents in regulating a variety of cellular processes including cell growth, cell death, and inflammation. The methods of the invention are useful for identifying compounds that have the ability to increase/decrease apoptosis, or comprise the ability to induce caspase

activation. The methods are useful for treating a disorder associated

CC with inappropriate apoptosis or inappropriate inflammation. The methods

CC are useful for treating disorders associated with an undesirably low rate

CC of apoptosis such as cancer (preferably follicular lymphoma, chronic

CC myelogenous leukaemia, melanoma, colon cancer, lung carcinoma, etc.),

CC viral infections, autoimmune diseases caused by low levels of apoptosis

CC (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis,

CC and arthritis). The methods are also useful for treating disorders with

CC undesirably high rates of apoptosis such as human immunodeficiency virus

CC (HIV) infection, Alzheimer's disease, Parkinson's disease, amyotrophic

CC lactic sclerosis (ALS), retinitis pigmentosa, spinal muscular atrophy,

CC various forms of cerebellar degeneration, naemia associated with chronic

CC disease, aplastic anaemia, chronic neutropenia, myelodysplastic

CC syndromes, myocardial infarction, stroke, and various inflammatory

CC disorders (e.g. Crohn's disease, reactive arthritis, insulin dependent

CC diabetes mellitus, multiple sclerosis, psoriasis, graft rejection,

CC allergic rhinitis, food allergies, conjunctivitis, glomerular nephritis,

CC etc). The present sequence represents human CARD-7
 XX Sequence 1429 AA;

Query Match	100.0%	Score 490;	DB 6;	Length 1429;
Best Local Similarity	100.0%	Pred. No.	2.2e-48;	
Matches	95;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

Qy 1 LHFVQREQLIARTSVEVVLKDKGQVLSQEYERVLAENTPSQMRKLFSLSQSWSDR 60
 Db 1335 LHFVQREQLIARTSVEVVLKDKGQVLSQEYERVLAENTPSQMRKLFSLSQSWSDR 1394

Qy 61 KCKDGLYQALKETHPHLIMELWEKGSKGLPLSS 95
 Db 1395 KCKDGLYQALKETHPHLIMELWEKGSKGLPLSS 1429

RESULT 9
 ABP96889 standard; protein: 1429 AA.
 ID ABP96889
 XX ABP96889 standard; protein: 1429 AA.
 AC AC 100.0%
 XX ABP96889;
 DT 16-JUN-2003 (first entry)
 XX Human caspase recruitment domain protein 7 SEQ ID NO:12.
 DB Human caspase recruitment domain protein 7 SEQ ID NO:12.
 XX ABP96889;
 KW Human; cytosolic; nootropic; neuroprotective; antiinflammatory;
 antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis;
 death effector filament-forming CBD4-like apoptosis protein;
 KW neurological disease; infection; inflammation; tumour formation;
 caspase recruitment domain protein 7.
 KW Homo sapiens.
 XX WO2003024988-A1.
 PN WO2003024988-A1.
 PD 27-MAR-2003.
 XX PR 19-SEP-2002; 2002WO-US029664.
 PF 19-SEP-2002; 2002WO-US029664.
 PA (ISIS-) ISIS PHARM INC.
 PI Bennett CF, Freier SM;
 XX DR 2003-354503/33.
 DR N-PSDB; ACC45152.
 XX PS Example 15; Page 121-128; 147pp; English.

The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding NAC, where the compound specifically hybridises with the nucleic acid molecule encoding NAC and inhibits the expression of NAC. The compound specifically hybridises with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding NAC. Also described: (1) a composition comprising (I) and a pharmaceutical carrier or diluent; (2) inhibiting the expression of NAC in cells or tissues comprising contacting the cells or tissues with (I); and (3) treating an animal having a disease or condition associated with NAC comprising administering (I) to the animal so that expression of NAC is inhibited. (I) has cytosolic, nootropic, neuroprotective and antiinflammatory activities, and can be used in antisense therapy. The antisense compounds (I) are useful for modulating the expression of NAC, and for treating a disease or condition associated with expression of NAC, e.g. hyperproliferative disease, neurological disease, or a disease or disorder arising from aberrant apoptosis. The compounds are also useful as research reagents and kits, or for diagnostics, therapeutics, and prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation. NAC is also known as a death effector filament-forming CED4-like apoptosis protein (DEFCAP). NAC is located on human chromosome 17p13. The present sequence represents a human caspase recruitment domain protein 7, which is used in an example from the invention.

Sequence 1429 AA;

Query Match	100.0%	Score 490;	DB 6;	Length 1429;
Best Local Similarity	100.0%	Pred. No.	2.2e-48;	
Matches	95;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

XX SQ Sequence 1429 AA;

Query Match

1 LHFVQREQLIARTSVEVVLKDKGQVLSQEYERVLAENTPSQMRKLFSLSQSWSDR 60	Score 490;	DB 6;	Length 1429;
Qy 1 LHFVQREQLIARTSVEVVLKDKGQVLSQEYERVLAENTPSQMRKLFSLSQSWSDR 60	Score 490;	DB 6;	Length 1429;
Db 1335 LHFVQREQLIARTSVEVVLKDKGQVLSQEYERVLAENTPSQMRKLFSLSQSWSDR 1394	Score 490;	DB 6;	Length 1429;

Qy 61 KCKDGLYQALKETHPHLIMELWEKGSKGLPLSS 95
 Db 1395 KCKDGLYQALKETHPHLIMELWEKGSKGLPLSS 1429

RESULT 10
 ABP96888
 ID ABP96888 standard; protein: 1429 AA.
 XX ABP96888;
 AC AC 100.0%
 XX ABP96888;
 DT 16-JUN-2003 (first entry)
 XX Human NAC protein SEQ ID NO:3.
 KW Human; cytostatic; nootropic; neuroprotective; antiinflammatory;
 antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis;
 death effector filament-forming CED4-like apoptosis protein;
 KW neurological disease; infection; inflammation; tumour formation;
 KW chromosome 17p13.
 DE Human NAC protein SEQ ID NO:3.
 KW Human; cytostatic; nootropic; neuroprotective; antiinflammatory;
 antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis;
 death effector filament-forming CED4-like apoptosis protein;
 KW neurological disease; infection; inflammation; tumour formation;
 KW chromosome 17p13.
 XX Homo sapiens.
 OS Homo sapiens.
 XX PN WO2003024988-A1.
 PN WO2003024988-A1.
 XX PR 27-MAR-2003.
 PD 27-MAR-2003.
 XX PR 19-SEP-2002; 2002WO-US029664.
 PR 19-SEP-2002; 2002WO-US029664.
 XX PR 19-SEP-2001; 2001US-00956712.
 PR 19-SEP-2001; 2001US-00956712.
 XX PA (ISIS-) ISIS PHARM INC.
 PA (ISIS-) ISIS PHARM INC.
 PI Bennett CF, Freier SM;
 XX DR 2003-354503/33.
 DR N-PSDB; ACC45152.
 XX PS Example 13; Page 81-88; 147pp; English.

The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding NAC, where the compound specifically hybridises with the nucleic acid molecule encoding NAC and inhibits the expression of NAC. The compound specifically hybridises with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding NAC. Also described: (1) a composition comprising (I) and a pharmaceutical carrier or diluent; (2) inhibiting the expression of NAC in cells or tissues comprising contacting the cells or tissues with (I); and (3) treating an animal having a disease or condition associated with NAC comprising administering (I) to the animal so that expression of NAC is inhibited. (I) has cytosolic, nootropic, neuroprotective and antiinflammatory activities, and can be used in antisense therapy. The antisense compounds (I) are useful for modulating the expression of NAC, and for treating a disease or condition associated with expression of NAC, e.g. hyperproliferative disease, neurological disease, or a disease or disorder arising from aberrant apoptosis. The compounds are also useful as research reagents and kits, or for diagnostics, therapeutics, and antisense compounds (I) are useful for modulating the expression of NAC, and can be used in antisense therapy. The antisense compounds (I) are useful for modulating the expression of NAC, and for treating a disease or condition associated with expression of NAC, e.g. hyperproliferative disease, neurological disease, or a disease or disorder arising from aberrant apoptosis. The compounds are also useful as research reagents and kits, or for diagnostics, therapeutics,

and for treating a disease or condition associated with expression of NAC, e.g. hyperproliferative disease, neurological disease, or a disease or disorder arising from aberrant apoptosis. The compounds are also useful as research reagents and kits, or for diagnostics, therapeutics and prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation. NAC is also known as a death effector filament-forming CED-1-like apoptosis protein (DECPAP). NAC is located on human chromosome 17p13. The present sequence represents human NAC, which is used in an example from the present invention.

XX Sequence 1429 AA;

Query Match	100.0%	Score 490; DB 6; Length 1429;
Best Local Similarity	100.0%	Pred. No. 2.2e-18;
Matches	95;	Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

RESULT 11

ABG71633 ABG71633 standard; protein; 1429 AA.
XX ID ABG71633;
AC AC

DT 10-JAN-2003 (first entry)
XX Human caspase recruitment domain-7 (CARD-7).

DE Human caspase activity; caspase recruitment domain-7; CARD-7; caspase-1; pseudo-interleukin-1 beta converting enzyme; IL-1beta; pseudo-ICE; ICBERBG; cell growth; cell death; inflammation; apoptosis; caspase activation; cancer; follicular lymphoma; leukaemia; melanoma; colon cancer; lung carcinoma; viral infection; autoimmune disease; systemic lupus erythematosus; reactive arthritis; human immunodeficiency virus infection; HIV infection; AIDS; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; myocardial infarction; stroke; inflammatory disorder; Crohn's disease; insulin dependent diabetes mellitus; multiple sclerosis; psoriasis; graft rejection; allergic rhinitis; food allergy; conjunctivitis; glomerular nephritis; cytostatic; vasoconstrictive; immunosuppressive; dermatological; nephrotropic; neuroprotective; cardiotropic.

XX Homo sapiens.

XX US2002128198-A1.

XX PD 12-SEP-2002.

XX PF 27-NOV-2001; 2001US-00936617.
XX PN 28-JUN-1999; 99US-00340620.
PR 27-OCT-1999; 99US-00428252.
PR 15-AUG-2001; 2001US-00931071.

XX PA (BERT) BERTIN J.

XX PI Bertin J;

XX DR WPI; 2003-028957/02.
N-PSD; ABS56030.

XX PT Identifying modulator of CARD-7 and CARD-5 interaction, by contacting CARD-7 and CARD-5 in presence of test compound, measuring their binding, and identifying modulator, when binding of CARD-7 to CARD-5 is altered.
XX Disclosure; Fig 1; 43pp; English.

XX

The present invention relates to methods of identifying compounds that regulate caspase activity using caspase recruitment domain-7 (CARD-7) or caspase recruitment domain-8 (CARD-8). In particular, method for identifying a compound that modulates the interaction between CARD-8 and caspase-1, pseudo-interleukin-1 (IL-1) beta converting enzyme (pseudo-ICE) or ICBERBG is disclosed. CARD-7 and CARD-8 molecules are useful as modulating agents in regulating a variety of cellular processes including cell growth, cell death, and inflammation. The methods of the invention are useful for identifying compounds that have the ability to increase/decrease apoptosis, or comprise the ability to induce caspase activation. The methods are useful for treating a disorder associated with inappropriate apoptosis or inappropriate inflammation. The methods are useful for treating disorders associated with an undesirably low rate of apoptosis such as cancer (preferably follicular lymphoma, chronic myelogenous leukaemia, melanoma, colon cancer, lung carcinoma, etc.), viral infections, autoimmune diseases caused by low levels of apoptosis (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis, and arthritis). The methods are also useful for treating disorders with undesirably high rates of apoptosis such as human immunodeficiency virus (HIV) infection, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS), retinitis pigmentosa, spinal muscular atrophy, various forms of cerebellar degeneration, anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, myelodysplastic syndromes, myocardial infarction, stroke, and various inflammatory disorders (e.g. Crohn's disease, reactive arthritis, insulin dependent diabetes mellitus, multiple sclerosis, psoriasis, graft rejection, allergic rhinitis, food allergies, conjunctivitis, glomerular nephritis, etc.). The present sequence represents human CARD-7.

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;
Best Local Similarity	100.0%;	Score 490; DB 6;
Matches	95;	Length 1429;
		Pred. No. 2.2e-48;
		Mismatches 0;
		Indels 0;
		Gaps 0;

Qy 1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60
Db 1335 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 1394

Qy 61 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 95
Db 1395 KCKDGLYQALKETHPLHIMLWEKGSKCQLPSS 1429

XX Sequence 1429 AA;

Query	1 LFHFVDQYREQLIARTSVEVLDKLHGQLSQEYRLAENTRPSQRKLSLSQSQWDR 60	Length 1429;

Location/Qualifiers	
FH	Key Binding-site
XX	FT FT
PF	/label= "ATP/GTP-binding_site"
XX	/note= "P-loop"
PR	FT FT
01-SEP-1999;	1216..1237
XX	/label= Transmembrane_domain
PA	XX
(BURNH-) BURNHAM INST.	WO200157085-A2.
XX	PN
Reed JC;	XX
XX	PD 09-AUG-2001.
WPI; 2001-18258/18.	XX
DR N-PDB; AAD02762.	PP 01-FEB-2001; 2001WO-US003455.
PT Novel nucleic acid encoding NB-ARC and caspase associated recruitment domains, used to produce polypeptides for screening for modulators of apoptosis.	XX 02-FEB-2000; 2000US-0180093P.
PT	PR 11-FEB-2000; 2000US-0182045P.
PS	XX (INCY-) INCYTE GENOMICS INC.
XX	XX
XX	XX Baughn MR, Au-Young J, Yue H;
CC	XX WPI; 2001-488869/53.
CC	DR N-PSDB; AAI12951.
CC	XX Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metabolic disorders.
CC	XX (INCY-) INCYTE GENOMICS INC.
CC	XX
CC	XX Claim 1: Page 114-117; 138pp; English.
CC	XX The present sequence is human G-protein coupled receptor-8 (GCRBC-8) protein. The present invention relates to GCREC protein and nucleic acids encoding them. GCREC protein, its agonist or antagonist are useful for treating diseases or conditions associated with decreased expression or overexpression of functional GCREC in a patient, where the disorder is selected from cell proliferative disorders such as acinic keratosis, CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and cancer, neurological disorders such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease, cardiovascular disorders such as hypertension, vasculitis, varicose veins, gastro-intestinal disorders such as dysphagia, dyspepsia, anaesthesia, CC pancytopenia, autoimmune/inflammatory disorders such as acquired CC immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease, CC uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections, trauma and metabolic disorders such as diabetes, obesity, CC osteoporosis. GCREC proteins and their cDNAs are used to assess the effects of exogenous compounds on the expression of GCREC sequences. CC GCREC cDNA is useful to create knock in humanised animals (pigs) or CC transgenic animals (mice or rats) to model human disease, for therapeutic CC or diagnostic purposes, for somatic or germinal gene therapy, to generate CC hybridisation probes useful in mapping the naturally occurring genomic CC sequence, and in molecular biological techniques
CC	XX Sequence 1442 AA:
CC	Sequence Match Score 100.0%; Score 490; DB 4; Length 1442;
CC	Best Local Similarity 100.0%; Pred. No. 2.2e-48;
CC	Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 LHFYDQYRQLIARTSVEVLDKLGQVLSQEYERTLAENTRPSQRKLFSLSQWDR 60
Do	1348 LHFYDQYRQLIARTSVEVLDKLGQVLSQEYERTLAENTRPSQRKLFSLSQWDR 1407
Qy	61 KCKDGlyQALKETHPHLIMELWEGSKKGLLPLSS 95
Db	1408 KCKDGlyQALKETHPHLIMELWEGSKKGLLPLSS 1442
RESULT 1.3	
AAE06755	AAE06758 standard; protein; 1473 AA.
ID	XX
AAE06758;	XX
XX	XX 16-OCT-2001 (first entry)
XX	Human G-protein coupled receptor-8 (GCREC-8) protein.
XX	Human; G-protein coupled receptor-8; GCREC-8; cytosatic; hepatotropic; virucidal; antiinflammatory; anticonvulsant; antiemetic; neuroprotective; otoprotective; cerebroprotective; hypotensive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis;
KW	anorectic; arteriosclerosis; atherosclerosis; diarrhoea; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; Huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia; anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder; Addison's disease; Crohn's disease; acquired immune deficiency syndrome; AIDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity; osteoporosis; transgenic animal; gene therapy.
KW	RESULT 1.4
KW	AAY72669
KW	ID AAY72669 standard; protein; 1473 AA.
XX	XX
AC	AC AAY72669;

DT 31-MAY-2001 (first entry)
 XX Human NB-ARC and CARD containing protein (NAC) beta isoform.
 DE Human: NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;
 KW caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;
 KW cysteine aspartyl protease; apoptosis; cytokine production;
 KW cytokine receptor signalling; therapy; inflammatory disorder; sepsis;
 KW fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.
 OS Homo sapiens.
 FH Key
 FT Domain
 /label= "NB domain
 /note= "Nucleotide binding domain, also designated as
 NB ARC domain"
 FT Domain
 /label= "Walker_A
 /note= "Also designated as P-loop"
 FT Domain
 /label= "Walker_B
 809 . 813
 FT Region
 /label= Leucine_rich_repeat_region
 838 . 862
 FT Region
 /label= Leucine_rich_repeat_region
 865 . 890
 FT Region
 /label= Leucine_rich_repeat_region
 895 . 919
 FT Region
 /label= Leucine_rich_repeat_region
 923 . 947
 FT Region
 /label= Leucine_rich_repeat_region
 957 . 987
 /note= "This 31 amino acid segment is not found in NAC
 gamma isoform (AY72670) and NAC delta isoform (AY72671)
 due to alternative mRNA splicing"
 FT Domain
 /note= "TIM-Barrel-like domain"
 FT Domain
 /label= CARD-L
 1128 . 1473
 FT Domain
 /label= "Caspase-associated recruitment domain"
 1128 . 1211
 FT Region
 /note= "CARD-S
 1261 . 1306
 /note= "This 45 amino acid segment is not found in NAC
 gamma isoform (AY72670) due to alternative mRNA
 splicing"
 FT Domain
 /label= CARD-S
 1306 . 1473
 /note= "Caspase-associated recruitment domain"
 FT Domain
 /label= CARD
 1373 . 1473
 /note= "Caspase-associated recruitment domain"
 FT XX
 PA WO200116170-A2.
 PD 08-MAR-2001.
 XX
 PR 01-SEP-2000: 2000WO-US024152.
 XX
 PR 01-SEP-1999: 99US-00388221.
 XX
 PA (BURN-) BURNHAM INST.
 PR
 PR Reed JC;
 XX
 DR WPI: 2001-183258/18.
 DR N-PSDDE; AddO2762.
 PR Novel nucleic acid encoding NB-ARC and caspase associated recruitment domains, used to produce polypeptides for screening for modulators of apoptosis.
 FT

XX Claim 15; Page 133-137; 184pp; English.
 PS XX
 CC The present sequence is a human NB-ARC and CARD containing protein (NAC) beta isoform. NAC splice variant in which both the splice regions are present in the translated polypeptide. NAC protein comprises a nucleotide binding (NB) domain (also referred as NB-ARC domain), a caspase-associated recruitment domain (CARD), and a TIM-Barrel-like domain. The caspases, cysteine aspartyl proteases, are principal effectors of apoptosis. CARD containing NAC proteins are used for screening modulators that modulates apoptosis, cytokine production, cytokine receptor signalling and other cellular processes. NAC can act as an immunogen for the production of polyclonal and monoclonal antibodies. It can also be used to diagnose and treat inflammatory disorders such as sepsis, fibrosis and arthritis. Note: This sequence is stated as being the same as that shown as SBQ ID NO:2 (AY72711) in figure 1A of the specification. However the sequences differ at several positions
 XX Sequence 1473 AA;
 SQ Query Match 100.0%: Score 490; DB 4; Length 1473;
 Best Local Similarity 100.0%; Pred. No 2.3e-48;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Qy 1 LHFVDQREQLIARYTSVEVVLDKLHGQVLSQEQQYERVLAAENTRSQMRLKFSLSQSWSWDR 60
 Db 1379 LHFVDQREQLIARYTSVEVVLDKLHGQVLSQEQQYERVLAAENTRSQMRLKFSLSQSWSWDR 1438
 CC
 Qy 61 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 95
 Db 1439 KCKDGLYQALKETHPHILMELWEKGSKKGLLPLSS 1473
 CC
 RESULT 15
 AAY72711
 ID AAY72711 standard; Protein; 1473 AA.
 XX
 AC AAY72711;
 XX
 DT 31-MAY-2001 (first entry)
 XX Human NAC beta isoform, alternative version.
 DE Human NAC beta isoform, alternative version.
 XX Human: NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;
 KW caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;
 KW cysteine aspartyl protease; apoptosis; cytokine production;
 KW cytokine receptor signalling; therapy; inflammatory disorder; sepsis;
 KW fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.
 XX Homo sapiens.
 Location/Qualifiers
 329 . 547
 /label= NB domain
 /note= "Nucleotide binding domain, also designated as NB-ARC domain"
 329 . 341
 /label= Walker_A
 /note= "Also designated as P-loop"
 406 . 414
 /label= Walker_B
 809 . 833
 /label= Leucine_rich_repeat_region
 838 . 862
 /label= Leucine_rich_repeat_region
 865 . 890
 /label= Leucine_rich_repeat_region
 895 . 919
 /label= Leucine_rich_repeat_region
 923 . 947
 /label= Leucine_rich_repeat_region
 957 . 987
 /label= Leucine_rich_repeat_region

FT /note= "This 31 amino acid segment is not found in NAC
FT gamma isoform (AAV72670) and NAC delta isoform (AAV72671)
FT due to alternative mRNA splicing"
FT Domain .1164
FT /note= "TMM-Barrel-like domain"
FT Domain .1473
FT /label= CARD-L
FT /note= "Caspase-associated recruitment domain"
FT Domain .1128 .1261
FT /label= CARD-S
FT /note= "Caspase-associated recruitment domain"
FT Region .1261 .1306
FT /note= "This 45 amino acid segment is not found in NAC
FT gamma isoform (AAV72670) due to alternative mRNA
FT splicing"
FT Misc-difference .1298 .1305
FT /note= "Encoded by GGATGCTGGAAATACTCCCCAAG"
FT Domain .1306 .1473
FT /label= CARD-S
FT /note= "Caspase-associated recruitment domain"
FT Domain .1373 .1473
FT /label= CARD
FT /note= "Caspase-associated recruitment domain"
XX WO200116170-A2.
XX PN
XX PD 08-MAR-2001.
XX PP 01-SEP-2000; 2000WO-US024152.
XX PR 01-SEP-1999; 99US-00388221.
XX PA (BURNHAM INST.
XX PI Reed JC;
XX DR 2001-1832556/18.
XX DR N-PSDB; AAD02760.
XX PT Novel nucleic acid encoding NB-ARC and caspase associated recruitment
PT domains, used to produce polypeptides for screening for modulators of
PT apoptosis.
XX Claim 15; Fig 1A; 184pp; English.
XX The present sequence is a human NB-ARC and CARD containing protein (NAC)
CC beta isoform, alternative version. NAC beta isoform represents the NAC
CC splice variant in which both the splice regions are present in the
CC translated polypeptide. NAC protein comprises a nucleotide binding (NB)
CC domain (CARD) and a TMM-Barrel-like domain. The caspases, cysteine
CC proteases, are principal effectors of apoptosis. CARD containing
CC proteins are used for screening modulators that modulates apoptosis,
CC cytokine production, cytokine receptor signalling and other cellular
CC processes. NAC can act as an immunogen for the production of polyclonal
CC and monoclonal antibodies. It can also be used to diagnose and treat
CC inflammatory disorders such as sepsis, fibrosis and arthritis and cancer
CC pathologies such as adenocarcinomas and leukaemias. Note: This sequence
CC is stated as being the same as that shown as SEQ ID NO:2 (See AAV72670)
CC in page 133-137 of the specification. However the sequences differ at
CC several positions
XX Sequence 1473 AA:
Query Match 100.0%; Score 490; DB 4; Length 1473;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LHFVDYREQLIARYTSVVEVLDKLHGQVLSQEQRVLAENTRSPQRKLFSLSQWDR 60
Db 1379 LHFVDYREQLIARYTSVVEVLDKLHGQVLSQEQRVLAENTRSPQRKLFSLSQWDR 1438
Qy 61 KCKDGLYQALKETHPHLIMELWEKGSKKGFLPLSS

GenCore version 5.1.6
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ON protein - protein search, using sw model

Run on: July 28, 2004, 08:46:11 ; Search time 41.0602 Seconds
 (without alignments)

Perfect score: 378
 Sequence: 1 GLHFIDQHRLALIARYTNVE.....LFSFTPANWTCIKLILQLQAL 71
 488.572 Million cells/sec

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqD1980s:*
- 2: geneseqD1990s:*
- 3: geneseqD2000s:*
- 4: geneseqD2001s:*
- 5: geneseqD2002s:*
- 6: geneseqD2003s:*
- 7: geneseqD2003Ds:*
- 8: geneseqD2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	%	Description
1	378	100.0	176	AAB00594	1	Aae00594 Alternat
2	378	100.0	195	2 AAY8553	1	Aay48553 Human bre
3	378	100.0	195	3 AAU8525	1	Aau68525 Human nov
4	378	100.0	195	4 AAB00585	1	Aab2571 Human CAR
5	378	100.0	195	4 AAB00588	1	Aae00588 Human tar
6	378	100.0	195	5 AAU9353	1	Aau9353 Human cas
7	378	100.0	195	5 AAC17854	1	Aao17854 Pyrin dom
8	378	100.0	195	6 ABG71635	1	Abg71635 Human cas
9	378	100.0	195	6 AAG74647	1	Aag74647 Human col
10	372	98.4	205	4 AAE00591	1	Aae00591 Hum tar
11	275	72.8	171	4 AAE00593	1	Aae00593 Rat targe
12	264	69.8	193	4 AAB20086	1	Aab20086 Mouse CAR
13	264	69.8	193	4 AAE00592	1	Aae00592 Mouse tar
14	264	69.8	193	5 AAU9352	1	Aau9352 Mouse cas
15	216	57.1	442	3 AAB24513	1	Aab24513 Human sec
16	216	57.1	1397	4 AAY2670	1	Aay72670 Human NB-
17	216	57.1	1429	4 AAB2571	1	Aab2571 Human CAR
18	216	57.1	1429	5 ABG78455	1	Abg78455 Human cas
19	216	57.1	1429	5 ABG78472	1	Abg78472 Leucine-r
20	216	57.1	1429	5 ABB77916	1	Abb77916 Human leu
21	216	57.1	1429	5 ABG7969	1	Abg7969 Human leu
22	216	57.1	1429	5 AAC017855	1	Aac017855 Pyrin dom
23	216	57.1	1429	6 ABG71631	1	Abg71631 Human cas
24	216	57.1	1429	6 ABP16889	1	Abp16889 Human cas
25	216	57.1	1429	6 ABP16888	1	Abp16888 Human NAC

ALIGNMENTS

26	216	57.1	1429	6 ABG71633	1	Abg71633 Human cas
27	216	57.1	1442	4 AAY72671	1	Aay72671 Human NB-
28	216	57.1	1473	4 AAE06758	1	Aae06758 Human G-P
29	216	57.1	1473	4 AAY7669	1	Aay7669 Human NB-
30	216	57.1	1473	4 AAY72711	1	Aay72711 Human NAC
31	214	56.6	190	3 AAB43675	1	Aab43675 Human can
32	214	56.6	190	3 AAB24519	1	Aab24519 Human sec
33	141	37.3	65	3 AAB24520	1	Aab24520 Human sec
34	75	59	3	4 ABJ04755	1	Abj04755 RRC prote
35	69.5	18.4	93	5 ABR58613	1	abr58613 Human can
36	69.5	18.4	208	6 ABR58613	1	abr58613 Human can
37	69.5	18.4	219	7 ADD48044	1	Add48044 Human Pro
38	68.5	18.1	230	4 AAU21812	1	Aau21812 Novel hum
39	68.5	18.1	230	7 ADC46453	1	Adc46453 Human neo
40	68.5	18.1	431	4 AAB62572	1	Aab62572 Human CAR
41	68.5	18.1	431	4 AAY72672	1	Aay72672 Human CAR
42	68.5	18.1	431	6 ABG71632	1	Abg71632 Human Cas
43	68.5	18.1	431	6 ABB82236	1	Abb82236 Human TUC
44	68.5	18.1	431	6 ABG71634	1	Abg71634 Human cas

RESULT 1
 AAE00594
 ID AAE00594 standard; protein; 176 AA.
 XX
 AC AAE00594;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Alternatively spliced form of human TMS1 protein (lacking exon).
 XX
 KW Human; target of methylation-induced silencing-1; TMS1; cytostatic;
 KW antiproliferative; apoptosis inducer; gene therapy; CPG island;
 KW caspase-recruiting domain; CARD; cancer; breast.
 XX
 OS Homo sapiens.
 XX
 PN WO200129235-A2.
 XX
 26-APR-2001.
 PD XX
 PR 18-OCT-1999;
 PR 18-OCT-1999; 99US-0159975P.
 XX
 (UYEM-) UNIV EMORY.
 XX
 PI Vertino PM;
 XX
 WPI; 2001-290922/30.
 DR XX
 DR N-PSDB; AAD0306.
 XX
 Novel gene TMS1 transcriptionally silenced due to increased methylation
 PT useful for identifying subject at risk of developing tumor characterized
 PT by abnormal methylation; for treating cancer by inducing apoptosis.
 XX
 PS Claim 85; Page 123; 124pp; English.
 XX
 The invention relates to identification of target of methylation-induced
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and plays
 CC a role in induction of apoptosis. TMS1 gene and protein are useful as
 CC tools for diagnosing and treating a subject at risk of developing tumor characterized
 CC (e.g. breast cancer) characterized by abnormal CpG methylation or
 CC abnormally low levels of TMS1 expression products. Unique fragments of
 CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1
 CC molecule is also useful for treating abnormal cell proliferation by
 CC increasing TMS1 polypeptide level to an above normal level. The
 CC Cpg

Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders thrombocytopenia, stem cell disorders, aplastic anaemia, for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, lung or liver fibrosis, repetitive injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions such as asthma or other respiratory problems, coagulation disorders, haemophilia, septic shock, sepsis, arthritis, nephritis and inflammatory bowel disease, viral infection and are useful in altering bodily characteristics. The present sequence represents a novel protein of the invention.

Sequence 195 AA:

Query Match	100	0%	Score 378;	DB 4;	Length 195;
Best Local Similarity	100	0%	Pred. No.	3.7e-40;	
Matches	71	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;

1 GLIFEDQHRAALIARVTVNEWLLDALYGYKVLTDQQAVTRAEPNTPSKMRKLFSFTPAWN 60

111 GLHFIIQHRAILARYTNNVWLLDALYKGKVLTDEQTAQVRAEPTNSSKMRKLFSFTPAWN 170
61 WTCKDQLLQL 71
171 WTCKDQLLQL 181

AAB2 0085 standard; protein: 195 AA.

AAB20085;

23-APR-2001 (first entry)

Human CARD-5 protein.

CARD-5; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; immune disease; inflammation.

immune disease; inflammation; anilinumour; anilseptic; immunomodulator; antinflammatory; apoptosis; diagnosis; gene therapy.

Homo sapiens.

key	Location/Qualifiers
Domain	111 . 181 /note= "CARD"

WO200100826-A2.

04-JAN-2001.

28-JUN-2000; 20000WO-US017691.

28-JUN-1999; 99US-00340620.

Bertin J: (MILL-) MILLENNIUM PHARM INC.

WPI; 2001-061973/07.

N-PSDB; AAP30007.

isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and caspase activations.

hematological disorders.

XX
PS Claim 9; Fig 21; 208PP; English.
XX
The present sequence is that of human caspase recruitment domain 5 (CARD-
CC 5), an intracellular protein predicted to be involved in regulating
CC caspase activation. The sequence is predicted from an isolated cDNA clone
CC (see AF30007). Methods of diagnosing and treating patients suffering
CC from a disorder associated with an abnormal level or rate of apoptotic
CC cell death, abnormal activity of the P_as/ApO-1 receptor complex, abnormal
CC activity of the tumour necrosis factor receptor complex or abnormal
CC activity of a caspase involve administering a compound that modulates the
CC expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using
CC gene therapy methods. Such disorders include cancer, viral infection,
CC autoimmune disorders, neurological diseases, haematological disorders,
CC inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6
CC proteins can be used to regulate cell proliferation, cell survival and
CC cell growth. They can also be used to screen drugs or compounds that
CC modulate their activity or expression and to treat disorders associated
CC with insufficient or excessive production of CARD-3, -4, -5 or -6
CC protein, or production of an aberrant protein
Sequence 195 AA:
SQ

Query Match 100.0%; Score 378; DB 4; Length 195;
 Best Local Similarity 100.0%; Pred. No. 3.7e-40;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GLHFIDQHRAALIARYTINVENMILDALYGVLTDEQYQAVRAEPTNFSKMRKLFSPTPAWN 60
Db	111	GLHFIDQHRAALIARYTINVENMILDALYGVLTDEQYQAVRAEPTNFSKMRKLFSPTPAWN 170
Qy	61	WTCKDILQLQAL 71
Db	171	WTCKDILQLQAL 181

RESULT 5
 AAE00588 standard; protein; 195 AA.
 AAE00588
 XX
 AC
 AC
 XX
 DT 02-JUL-2001 (first entry)
 DE Human target of methylation-induced silencing-1 (TMS1) protein.
 KW Human; target of methylation-induced silencing-1; TMS1; Cystostatic;
 KW antiproliferative; apoptosis inducer; Gene therapy; CpG island;
 KW caspase-recruiting domain; CARD; cancer; breast.
 KW Homo sapiens.
 OS WO200129235-A2.
 XX
 PN 26-APR-2001.
 XX
 PR 18-OCT-2000; 2000WO-US028747.
 XX
 PR 18-OCT-1999; 99US-0159975P.
 XX
 PR (UYEM-) UNIV EMORY.
 PI Vertino PM;
 XX
 DR WPI; 2001-290922/30.
 DR N-PSDB; AAD03889, AAD03890.
 XX
 PR Novel gene TMS1, transcriptionally silenced due to increased methylation
 PT useful for identifying subject at risk of developing tumor characterized
 PT by abnormal methylation, for treating cancer by inducing apoptosis.
 XX
 XX
 Claim 85; Page 114; 124PP; English.

The invention relates to identification of target of methylation-induced silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to abnormal methylation of a CDS region in its 5' regulatory region. TMS1 consists of a carboxy terminal caspase-recruiting domain (CARD) and plays a role in induction of apoptosis. TMS1 gene and protein are useful as tools for diagnosing and treating a subject at risk of developing cancer (e.g., breast cancer) characterised by abnormal CpG methylation or abnormally low levels of TMS1 expression products. Unique fragments of TMS1 genes are used as probes. TMS1 gene is useful in gene therapy. TMS1 molecule is also useful for treating abnormal cell proliferation by increasing TMS1 polypeptide level to an above normal level. The CDS island region of TMS1 or its fragments are used to study the methylation patterns apart from any coding region contained in it. The present sequence is human target of methylation-induced silencing-1 (TMS1)

Sequence 195 AA;

Query Match 100.0%; Score 378; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 3..7e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLHFIDQHRAILARYNTNVEWLDDALYGYVLTDQYQAVRAEPTNPNSMRKLFSTPAWN 60
Db 111 GLHFIDQHRAILARYNTNVEWLDDALYGYVLTDQYQAVRAEPTNPNSMRKLFSTPAWN 170
Qy 61 WTCKDILQLQAL 71
Db 171 WTCKDILQLQAL 181

RESULT 6

AAU9353 standard; protein; 195 AA.
ID AAU9353
XX AC AAU9353;
XX DT 07-OCT-2002 (first entry)

XX Human caspase recruitment domain-5 (CARD-5) protein.

DB Human; caspase recruitment domain-5; CARD-5; antiinflammatory; immunosuppressive; caspase; cysteine1 aspartate-specific Proteinase; apoptosis; nuclear factor-kappa B; NF-kappaB; transcription factor; cell proliferation; gene therapy; immune disorder; chronic inflammatory disease; asthma; allergy; Hashimoto's disease; sarcoidosis; atopy; cell depletion; neurological disorder; Alzheimer's disease; human immunodeficiency virus; HIV; bacterial infection; leprosy; leprosy; sarcoidosis; cell depletion; neurological disorder; Alzheimer's disease; Parkinson's disease; spinal muscular atrophy; haematologic disease; myelodysplastic syndrome; aplastic anaemia; myocardial infarction; stroke.

XX OS Homo sapiens.

XX Key Location/Qualifiers
FT 1..195
FT /label= CARD_domain

XX PN WO200244354-A2.

XX PD 06-JUN-2002.

XX 29-NOV-2001; 2001WO-US044894.
XX 01-DEC-2000; 2000US-00728721.

PR 24-APR-2001; 2001US-00841879.

PA (MILLI-) MILLENION PHARM INC.

XX PI Bertin J;

DR WPI; 2002-557338/59.
DR N-PSDB; ABR8796.

XX Novel isolated murine or human caspase recruitment domain (CARD)-5 polypeptide, useful for treating immune disorders such as Hashimoto's thyroiditis, graft rejection, allergy, glomerular nephritis, PT tuberculosis.

XX Claim 22; Fig 3; 100pp; English.

XX PS

XX The invention discloses the isolated polypeptides, and encoding nucleic acids, of murine and human caspase recruitment domain (CARD)-5. Caspases (cysteinyl aspartate-specific proteases) are central to the apoptotic program and responsible for the degradation of cellular proteins that lead to the morphological changes seen in cells undergoing apoptosis.

XX Caspases interact with other caspases via their CARDs and different

CC subtypes of CARDs may confer binding specificity. CARD-5 is an intracellular protein that is predicted to be involved in regulating

CC caspase activation. CARD-5 activates the nuclear factor-kappa B (NF-

CC kappaB) transcription factor pathway and binds the CARDs of caspase-1, CC CARD-7 and itself. CARD-5 can, therefore, modulate CARD-5 activity and NF-

CC -kappaB activation; regulate cell growth and cell death and be used in CC gene therapy. The CARD-5 polypeptides are useful for identifying CC compounds which bind to them and modulate their activity and for CC detecting the presence of CARD-5 in a sample. CARD-5 polymersides, CC nucleic acids, antibodies and modulators of CARD-5 expression or activity CC can be used to treat immune disorders such as chronic inflammatory CC diseases and disorders, Hashimoto's thyroiditis, graft rejection, CC sarcoidosis, atopic conditions (such as asthma and allergy), Glomerular CC nephritis, human immunodeficiency virus (HIV) and bacterial infections CC (including tuberculosis and leprosy), and in screening and CC detection assays. Modulators of CARD-5 activity or expression are also CC useful for treating autoimmune disorders, such as systemic lupus erythematosus and arthritis, cell depletion, neurological disorders, such CC as Alzheimer's disease, Parkinson's disease and spinal muscular atrophy, CC haematologic diseases, such as myelodysplastic syndrome and aplastic CC anaemia, myocardial infarction and stroke. The sequence presented is the CC human caspase recruitment domain-5 (CARD-5) protein.

XX SQ Sequence 195 AA;

Query Match 100.0%; Score 378; DB 5; Length 195;
Best Local Similarity 100.0%; Pred. No. 3..7e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAILARYNTNVEWLDDALYGYVLTDQYQAVRAEPTNPNSMRKLFSTPAWN 60

Db 111 GLHFIDQHRAILARYNTNVEWLDDALYGYVLTDQYQAVRAEPTNPNSMRKLFSTPAWN 170

Qy 61 WTCKDILQLQAL 71

Db 171 WTCKDILQLQAL 181

RESULT 7

AAO17854

XX ID AAO17854 standard; protein; 195 AA.

AAO17854;

XX AC

XX DT 20-AUG-2002 (first entry)

XX Pyrin domain containing protein Pycard.

XX PD XX Pyrin domain, PYD domain, antiinflammatory; antiParkinsonian;

XX F1 XX antiarrhythmic; antipsoriatic; antibacterial; virucide;

XX FT XX neuroprotective; antiarthritic; antirheumatic; antiasthmatic;

XX PR XX nephroprotective; osteoprotective; nocropic; intracellular signal transduction;

XX PA XX inflammation; Alzheimer's disease; infection; psoriasis; asthma;

XX (MILLI-) MILLENION PHARM INC.

XX PA multiple sclerosis; rheumatoid arthritis; sarcoidosis;

XX PI osteoarthritis; glomerulonephritis.

OS Unidentified.

XX WO200240668-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 30-OCT-2001; 2001WO-EPO12545.
 XX
 PR 15-NOV-2000; 2000DE-0105687.
 PR 30-NOV-2000; 2000DE-0105959.
 XX
 PA (APOT-) APOTECH RES & DEV LTD.
 XX
 PI TSCHOPP J, Martinon F;
 XX
 DR WPI; 2002-427093/45.
 XX
 DR N-PSDB; AAL47126.
 XX
 PT New DNA encoding protein with pyrin domain, useful for treating diseases involving impaired signal transduction, particularly inflammation, also proteins and antibodies.
 PT
 XX
 PS Claim 5; Fig 1; 116pp; German.
 XX
 CC The present invention relates the DNA and their encoded Proteins, where the proteins contain at least one PYD (pyrin) domain. These can be used to treat diseases associated with impaired intracellular signal transduction, particularly inflammation such as Psoriasis, arteriosclerosis, bacterial or viral infections (particularly meningitis and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma, sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's disease and Parkinson's diseases. The present sequence is a protein of the invention
 CC Sequence 195 AA;
 SQ Query Match 100.0%; Score 378; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 3.7e-40;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GLHFIDQHAAALLIARYTIVNWLDDALYGVLTDBQYQAVRAEPTNPSMRKLFSTPAWN 60
 Db 111 GLHFIDQHAAALLIARYTIVNWLDDALYGVLTDBQYQAVRAEPTNPSMRKLFSTPAWN 170
 Qy 61 WTCKDLQL 71
 Db 171 WTCKDLQL 181
 RESULT 8
 ABG71635 standard; protein; 195 AA.
 ID ABG71635
 XX
 AC ABG71635;
 DT 10-JAN-2003 (first entry)
 XX
 DE Human caspase recruitment domain-5 (CARD-5).
 XX
 KW Human; caspase activity; caspase recruitment domain-5; CARD-5; caspase-1; caspase-1; caspase-1 beta converting enzyme; IL-1beta; PseudoICE; PseudoICE; cell growth; cell death; inflammation; CARD-7; apoptosis; caspase activation; cancer; follicular lymphoma; leukaemia; melanoma; colon cancer; lung carcinoma; viral infection; autoimmune disease; systemic lupus erythematosus; reactive arthritis; human immunodeficiency virus infection; HIV infection; AIDS; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; myocardial infarction; stroke; inflammatory disorder; Crohn's disease; insulin dependent diabetes mellitus; multiple sclerosis; psoriasis; graft rejection; Glomerular nephritis; allergic rhinitis; food allergies; conjunctivitis; dermatological; nephrotropic; neuroprotective; cardiant; caspase recruitment domain-7.
 XX
 OS Homo sapiens.
 XX
 PN US2002128198-A1.
 XX
 PD 12-SEP-2002.
 XX
 PF 27-NOV-2001; 2001US-00996617.
 XX
 PR 28-JUN-1999; 99US-00340620.
 PR 27-OCT-1999; 99US-00428252.
 PR 15-AUG-2001; 2001US-00931071.
 XX
 PA (BERT/) BERTIN J.
 PA
 PI Bertin J;
 XX
 WPI; 2003-028967/02.
 DR N-PSDB; ABS56032.
 XX
 PT Identifying modulator of CARD-7 and CARD-5 interaction, by contacting CARD-7 and CARD-5 in presence of test compound, measuring their binding, and identifying modulator, when binding of CARD-7 to CARD-5 is altered.
 XX
 PT Disclosure; Fig 7; 43pp; English.
 XX
 CC The present invention relates to methods of identifying compounds that regulate caspase activity using caspase recruitment domain-7 (CARD-7) or caspase recruitment domain-8 (CARD-8). In particular, a method for identifying a compound that modulates the interaction between CARD-8 and caspase-1, pseudo-interleukin 1 (IL-1) beta converting enzyme (pseudoICE) or ICEBERG is disclosed. CARD-7 and CARD-8 molecules are useful as modulating agents in regulating a variety of cellular processes including cell growth, cell death, and inflammation. The methods of the invention are useful for identifying compounds that have the ability to increase/decrease apoptosis, or comprise the ability to induce caspase activation. The methods are useful for treating a disorder associated with inappropriate apoptosis or inappropriate inflammation. The methods are useful for treating disorders associated with an undesirably low rate of apoptosis such as cancer (preferably follicular lymphoma, chronic myelogenous leukaemia, melanoma, colon cancer, lung carcinoma, etc.), viral infections, autoimmune diseases caused by low levels of apoptosis (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis, etc.). The methods are also useful for creating disorders with undesirably high rates of apoptosis such as human immunodeficiency virus (HIV) infection, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS), retinitis pigmentosa, spinal muscular atrophy, various forms of cerebellar degeneration, anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, myelodysplastic syndromes, myocardial infarction, stroke, and various inflammatory disorders (e.g. Crohn's disease, reactive arthritis, insulin dependent diabetes mellitus, multiple sclerosis, psoriasis, graft rejection, allergic rhinitis, food allergies, conjunctivitis, Glomerular nephritis, etc.). The present sequence represents human CARD-5. The sequence encoding CARD-5 is used to identify cDNA encoding CARD-7
 XX
 SQ Sequence 195 AA;
 SQ Query Match 100.0%; Score 378; DB 6; Length 195;
 Best Local Similarity 100.0%; Pred. No. 3.7e-40;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GLHFIDQHAAALLIARYTIVNWLDDALYGVLTDBQYQAVRAEPTNPSMRKLFSTPAWN 60
 Db 111 GLHFIDQHAAALLIARYTIVNWLDDALYGVLTDBQYQAVRAEPTNPSMRKLFSTPAWN 170
 Qy 61 WTCKDLQL 71
 Db 171 WTCKDLQL 181
 RESULT 9
 AAG74547
 ID AAG74547 standard; protein; 205 AA.
 XX

KW antiproliferative; apoptosis inducer; gene therapy; CpG island;
 KW caspase-recruiting domain; CARD; cancer; breast.

Rattus norvegicus.

Key Misc-difference 36
 /note= "Encoded by AGY"

WC200129235-A2.

PD 26-APR-2001.

XX 18-OCT-2000; 2000WO-US028747.

XX 18-OCT-1999; 99US-0159975P.

PA (UYEM-) UNIV EMORY.

PI Vertino PM;

XX DR WPI; 2001-290922/30.

DR N-PSDB; AAD03905.

Novel gene TMS1, transcriptionally silenced due to increased methylation useful for identifying subject at risk of developing tumor characterized by abnormal methylation, for treating cancer by inducing apoptosis.

PS Claim 85; Page 121; 124pp; English.

CC The invention relates to identification of target of methylation-induced silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and plays CC a role in induction of apoptosis. TMS1 gene and protein are useful as tools for diagnosis and characterising a subject at risk of developing cancer (e.g. breast cancer) characterised by abnormal CpG methylation or CC abnormally low levels of TMS1 expression products. Unique fragments of CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1 molecule is also useful for treating abnormal cell proliferation by increasing TMS1 polypeptide level to an above normal level. The CpG CC island region of TMS1 or its fragments are used to study the methylation patterns apart from any coding region contained in it. The present CC sequence is rat target of methylation-induced silencing-1 (TMS1) partial protein.

XX Sequence 171 AA:

Query Match 72.8%; Score 275; DB 4; Length 171;

Best Local Similarity 76.8%; Pred. No. 5.4e-27; Mismatches 6; Indels 0; Gaps 0;

Matches 53; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

SQ 3 HFIDQHRAALIARYTVNWLDAVGYLTDEQYQAVRAEPTNSKMRKLFSFTPANNWT 62

Db 89 HFIDQHRAALIARYTVNWLDAVGYLTDEQYQAVRAEPTNSKMRKLFSFTPANNWT 148

Qy 63 CKDLILQL 71

Db 149 CRNLFLEAL 157

RESULT 12
 AAB20086
 ID AAB20086 standard; protein; 193 AA.
 XX
 AC AAB20086;
 AC

DT 23-APR-2001 (first entry)
 XX
 DE Mouse CARD-5 protein.
 XX
 KW autoimmunity disease; neurological disease; mouse; cancer; infection;

KW autoimmune disease; haematological disease;

KW immune disease; inflammation; antitumour; anti-septic; immunomodulator;
 KW antiinflammatory; apoptosis; diagnosis; gene therapy.

OS Mus sp.

Key Location/Qualifiers
 Misc-difference 36
 /note= "Encoded by AGY"

PN WC200100826-A2.

PD 04-JAN-2001.

XX 28-JUN-2000; 2000WO-US017691.

XX 28-JUN-1999; 99US-00340620.

XX (MILL-) MILLENIUM PHARM INC.

PA Bertin J;

XX PI Bertin J;

XX DR WPI; 2001-061973/07.

DR N-PSDB; AAF30006.

XX Isolated intracellular proteins predicted to be involved in regulating PT caspase activation are used for diagnosis and treatment of e.g. cancer, PT viral infections, autoimmune diseases, neurological diseases and PT hematological disorders.

XX Claim 9; Fig 19; 204pp; English.

CC The present sequence is that of mouse caspase recruitment domain 5 (CARD-5), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAF30008). It shows 71% amino acid identity to human CARD-5 (see AAB20085). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the tumour necrosis factor receptor compound or abnormal expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using gene therapy methods. Such disorders include cancer, viral infection, autoimmune disorder, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6 proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein.

XX Sequence 193 AA;

Query Match 69.8%; Score 264; DB 4; Length 193;

Best Local Similarity 73.9%; Pred. No. 1.6e-25; Mismatches 7; Indels 0; Gaps 0;

Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 3 HFIDQHRAALIARYTVNWLDAVGYLTDEQYQAVRAEPTNSKMRKLFSFTPANNWT 62

Db 111 HFIDQHRAALIARYTVNWLDAVGYLTDEQYQAVRAEPTNSKMRKLFSFTPANNWT 170

Qy 63 CKDLILQL 71

Db 171 CKDLILQL 179

RESULT 13

AAB00592
 ID AAB00592 standard; protein; 193 AA.
 XX
 AC AAB00592;
 AC

DT 02-JUL-2001 (first entry)

XX

QY 3 HFIDQHRAALIARYTNVENVILDALYKGKLTDEQYQAVRAEPTNSKMRKLFSFTPAWNWT 62
 DB 111 HFVDQHRAALIARYTNVENVILDALYKGKLTDEQYQAVRAEPTNSKMRKLFSFTPAWNWT 61
 QY 63 CKDILQLAL 71
 DB 171 CKDILQLAL 179

RESULT 15
 AAB24513 standard; protein: 442 AA.
 AC AAB24513;
 XX DT 20-NOV-2000 (first entry)
 DE Human secreted protein sequence encoded by gene 12 SEO ID NO:139.
 XX Human; secreted protein; cytosstatic; antianaemic; antirheumatic; antiarthritic;
 KW antiinflammatory; ophthalmological; cardiotonic; anti-HIV; nootropic;
 KW antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic;
 KW neutroprotective; antimicrobial; antiparkinsonian; cancer; cancer;
 KW immune system disorder; angiogenesis; hyperproliferative disorder;
 KW cardiovascular disorder; apoptosis; neurological disease;
 KW infection disease; wound healing.
 XX Homo sapiens.
 OS XX
 PN WC20003537-A1.
 XX PD 22-JUN-2000.
 XX PF 16-DEC-1999; 99MO-US029950.
 XX PR 17-DEC-1998; 98US-0112809P.
 XX PR 18-DEC-1998; 98US-0113006P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;
 Duan DR, Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence K;
 XX DR 2000-431566/37.
 XX PT Forty seven human nucleic acids encoding secreted proteins, useful in the
 PT treatment, prevention and diagnosis of cancers, disorders of the immune
 PT system, angiogenesis, disorders, neurological diseases and
 PT hyperproliferative disorders.

PS Disclosure: Page 37; 562pp; English.

CC The polynucleotide sequence given in AAA78381 to AAA78432 encode the
 CC human secreted proteins given in AAB24437 to ABB24604. Human secreted
 CC proteins have activities based on the tissues and cells the genes are
 CC expressed in. Examples of activities include: cytostatic; antianaemic;
 CC antiinflammatory; ophthalmological; antiarthritic; antiheumatic;
 CC antipsoriatic; antiangiogenic; cardiant; anti-HIV;
 CC nootropic; neuroprotective; antimicrobial and antiparkinsonian. Human
 CC secreted protein polyaminoacides, polypeptides, antagonists and/or
 CC agonists may be useful in treating, preventing, and/or diagnosing other
 CC diseases, disorders, and/or conditions such as (a) cancers; (b)
 CC disorders of the immune system; (c) angiogenesis; (d) diseases
 CC associated with hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases
 CC associated with increase apoptosis; (g) neurological diseases; and
 CC (h) infectious diseases. They are also used to promote wound healing.
 CC AAA78372 to AAA78380 and AAB24436 represent sequences used in the
 CC exemplification of the present invention

SQ Sequence 442 AA;

Query Match

57.1%; Score 216; DB 3; Length 442;

Qy Best Local Similarity 61.4%; Pred. No. 6.8e-19; Mismatches 12;保守性 43; Indels 0; Gaps 0;
 Matches 339 LHFIDQHRAALIARYTNVENVILDALYKGKLTDEQYQAVRAEPTNSKMRKLFSFTPAWNWT 61
 Qy 2 LHFIDQHRAALIARYTNVENVILDALYKGKLTDEQYQAVRAEPTNSKMRKLFSFTPAWNWT 62
 Db 339 LHFIDQHRAALIARYTNVENVILDALYKGKLTDEQYQAVRAEPTNSKMRKLFSFTPAWNWT 61
 Qy 62 TCKDILQLAL 71
 Db 399 KCKDGLYQAL 408

Search completed: July 28, 2004, 08:53:00
 Job time : 41.0602 secs



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OM protein - protein search, using sw mode1

Run on: July 26, 2004, 08:51:17 ; Search time 12:40:36 Seconds
(without alignments)

295.514 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181

Perfect score: 1 GLHFIDQHRAALIARYTNE.....LFSFTPAWNWTCIKILLQAL 71

Sequence: /

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 369414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

369414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgr2_6/ptodata/2/iaa/5B_COMBO.PEP:*

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4: /cgr2_6/ptodata/2/iaa/6B_COMBO.PEP:*

5: /cgr2_6/ptodata/2/iaa/PCTUS_COMBO.PEP:*

6: /cgr2_6/ptodata/2/iaa/backfile1.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	71	4 US-09-340-620A-58	Sequence 58, Appl
2	378	100.0	195	4 US-09-340-620A-49	Sequence 49, Appl
3	264	67.8	70	4 US-09-340-620A-57	Sequence 57, Appl
4	264	69.8	193	4 US-09-340-620A-66	Sequence 66, Appl
5	264	69.8	109	4 US-09-340-620A-61	Sequence 61, Appl
6	13.0	34.5	106	4 US-09-069-023-10	Sequence 10, Appl
7	69.5	18.4	208	4 US-09-069-023-8	Sequence 8, Appl
8	69.5	18.4	221	4 US-09-069-023-22	Sequence 22, Appl
9	69.5	17.3	94	4 US-09-099-021-31	Sequence 31, Appl
10	65.5	17.3	94	4 US-09-245-281-31	Sequence 31, Appl
11	65.5	17.3	94	4 US-09-207-359B-31	Sequence 31, Appl
12	65.5	17.3	94	4 US-09-340-620A-31	Sequence 31, Appl
13	65.5	17.3	94	4 US-09-865-364-31	Sequence 31, Appl
14	65.5	17.3	94	4 US-09-099-041A-10	Sequence 10, Appl
15	64.5	17.1	100	4 US-09-245-281-10	Sequence 10, Appl
16	64.5	17.1	100	4 US-09-207-359B-10	Sequence 10, Appl
17	64.5	17.1	100	4 US-09-340-620A-10	Sequence 10, Appl
18	64.5	17.1	100	4 US-09-865-364-10	Sequence 10, Appl
19	64.5	17.1	164	4 US-09-245-281-41	Sequence 41, Appl
20	64.5	17.1	164	4 US-09-207-359B-41	Sequence 41, Appl
21	64.5	17.1	164	4 US-09-340-620A-41	Sequence 41, Appl
22	64.5	17.1	164	4 US-09-865-364-41	Sequence 41, Appl
23	64.5	17.1	249	4 US-09-245-281-39	Sequence 39, Appl
24	64.5	17.1	249	4 US-09-207-359B-39	Sequence 39, Appl
25	64.5	17.1	249	4 US-09-340-620A-39	Sequence 39, Appl
26	64.5	17.1	249	4 US-09-865-364-39	Sequence 39, Appl
27	64.5	17.1	450	3 US-09-019-942-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-340-620A-58
; Sequence 58, Application US/09340620A
; Patent No. 6432933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340-620A-58
; PRIORITY FILING DATE: 1999-06-28
; PRIORITY APPLICATION NUMBER: US 09/245-281-5
; PRIORITY FILING DATE: 1999-02-05
; PRIORITY APPLICATION NUMBER: US 09/207-359
; PRIORITY FILING DATE: 1998-12-08
; PRIORITY APPLICATION NUMBER: US 09/099, 041
; PRIORITY FILING DATE: 1998-06-17
; PRIORITY APPLICATION NUMBER: US 09/019, 942
; PRIORITY FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-58

Query Match 100.0%; Score 378; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 1; 5E-42;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIARYTNEVILDALYGVLTDEQYAVRAEPTNSPKMRKLFSPPTPAWN 60
Db 1 GLHFIDQHRAALIARYTNEVILDALYGVLTDEQYAVRAEPTNSPKMRKLFSPPTPAWN 60

RESULT 2
US-09-340-620A-49
; Sequence 49, Application US/09340620A
; Patent No. 6432933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340-620A-49
; PRIORITY FILING DATE: 1999-06-28
; PRIORITY APPLICATION NUMBER: US 09/245-281

PRIOR FILING DATE: 1999-02-05
 PRIOR APPLICATION NUMBER: US 09/207, 359
 PRIOR FILING DATE: 1998-12-08
 PRIOR APPLICATION NUMBER: US 09/099, 041
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: US 09/019, 942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 71
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 49
 LENGTH: 195
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-340-620A-49

Query Match 100.0%; Score 378; DB 4; Length 195;
 Best Local Similarity 100.0%; Pred. No. 5.4e-42; Indels 0; Gaps 0;
 Matches 71; Conservative 0; Mismatches 0; Gaps 0;
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-340-620A-66

Qy 1 GLHFIDQRHALLARYTNTVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 60
 Db 111 GLHFIDQRHALLARYTNTVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 170

Qy 61 WTCKDLIQL 71
 Db 171 WTCKDLIQL 181

RESULT 3
 US-09-340-620A-57
 Sequence 57, Application US/09340620A
 Patent No. 6482933

GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07334-124001
 CURRENT APPLICATION NUMBER: US/09/340, 620A
 CURRENT FILING DATE: 1999-06-28
 PRIORITY NUMBER: US 09/245, 281
 PRIOR FILING DATE: 1999-02-05
 PRIORITY NUMBER: US 09/207, 359
 PRIOR FILING DATE: 1998-12-08
 PRIORITY NUMBER: US 09/099, 041
 PRIOR FILING DATE: 1998-06-17
 PRIORITY NUMBER: US 09/019, 942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 71
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 57
 LENGTH: 70
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-340-620A-57

Query Match 69.8%; Score 264; DB 4; Length 70;
 Best Local Similarity 73.9%; Pred. No. 1.6e-27; Indels 0; Gaps 0;
 Matches 51; Conservative 7; Mismatches 11; Gaps 0;

Qy 3 HFIDQHALLARYTNTVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 62
 Db 2 HFVDQHQLARRYTNTVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 61

Qy 63 CKDLIQL 71
 Db 62 CKDSLQAL 70

RESULT 5
 US-09-340-620A-61
 Sequence 61, Application US/09340620A
 Patent No. 6482933

GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07334-124001
 CURRENT APPLICATION NUMBER: US/09/340, 620A
 CURRENT FILING DATE: 1999-06-28
 PRIORITY NUMBER: US 09/245, 281
 PRIOR FILING DATE: 1999-02-05
 PRIORITY NUMBER: US 09/207, 359
 PRIOR FILING DATE: 1998-12-08
 PRIORITY NUMBER: US 09/099, 041
 PRIOR FILING DATE: 1998-06-17
 PRIORITY NUMBER: US 09/019, 942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 71
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 61

Query Match 69.8%; Score 264; DB 4; Length 193;
 Best Local Similarity 73.9%; Pred. No. 5.7e-27; Indels 0; Gaps 0;
 Matches 51; Conservative 7; Mismatches 11; Gaps 0;

Qy 3 HFIDQHALLARYTNTVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 62
 Db 2 HFVDQHQLARRYTNTVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 61

Qy 63 CKDLIQL 71
 Db 171 CKDSLQAL 179

RESULT 6

US-09-340-620A-66
 Sequence 66, Application US/09340620A
 Patent No. 6482933

GENERAL INFORMATION:
 APPLICANT: Bertin, John

US-09-340-620A-71
i Sequence 71, Application US/09340620A
i GENERAL INFORMATION:
i APPLICANT: Berlin, John
i TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
i FILE REFERENCE: 07334-124001
i CURRENT APPLICATION NUMBER: US/09/340,620A
i PRIOR APPLICATION NUMBER: US 09/245,281.
i PRIOR FILING DATE: 1999-02-05
i PRIORITY NUMBER: US 09/247,359
i PRIOR FILING DATE: 1998-12-08
i PRIOR APPLICATION NUMBER: US 09/099,041.
i PRIOR FILING DATE: 1998-06-17
i PRIOR APPLICATION NUMBER: US 09/019,942
i PRIOR FILING DATE: 1998-02-06
i NUMBER OF SEQ ID NOS: 71
i SOFTWARE: FastSEQ for Windows Version 4.0
i SEQ ID NO: 71
i LENGTH: 109
i TYPE: PRT
i ORGANISM: Artificial Sequence
i FEATURE:
i OTHER INFORMATION: Consensus sequence
i NAME/KEY: VARIANT
i LOCATION: (1) ..(109)
i OTHER INFORMATION: Xaa = Any Amino Acid

US-09-340-620A-71
Qy 1 GLHFIDQHRAALIARVTN--VENVILDALYQK-VLTDEQYQAVRAEPTNSKMRKLFSFTP 57
Db 7 GSEI1DORHXALLARVTNPDXSLLDALLSRDLJSEEDEYAEAEITVLSKVRLLIVQ 66

Qy 58 A-WWNTCKDL--LQL 71
Db 67 SKGEETCKFLKCLLQAL 84

US-09-069-023-10
Qy 1 Sequence 10, Application US/09069023A
i GENERAL INFORMATION:
i APPLICANT: Inohara, Naohiro
i APPLICANT: Koseki, Takeyoshi
i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
i FILE REFERENCE: UM-03333
i CURRENT APPLICATION NUMBER: US/09/069,023A
i CURRENT FILING DATE: 1998-04-27
i NUMBER OF SEQ ID NOS: 38
i SOFTWARE: Patentin Ver. 2.0
i SEQ ID NO: 10
i LENGTH: 106
i TYPE: PRT
i ORGANISM: Homo sapiens

US-09-069-023-10
Qy 5 IDQHRAALIARV-TNVEWLDALYQK-VLTDEQYQAVRAEPTNSKMRKLFSFT----- 56
Db 12 IDRERKLVETLQADSGLLDALLARGVLTGPEYEALDLPDAERRVRRLILVQSKGEA 71

Qy 57 -----PAWW 61
Db 72 ACQELLRGQQTVSMPDFAWDW 93

RESULT 1.0

RESULT 14
US-09-865-364-31
Sequence 31; Application US/09865364
Patent No. 6613521
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865-364
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 31
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
US-09-865-364-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;
Best Local Similarity 25.9%; Pred. No. 0.34;
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;
6 DQHRAALIARY-TNVEMLLDALYGK-VLTDEQYOAVERAEPTNPSKMRKLFSFT----- 56
| : | : ; : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 10 DRERKRLVETLQADSGLLDALLARGVLTGPEALDALPDAERRVRLLLYQKGEEA 69
Qy 57 -----PAANNW 61
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 70 CQEILRCAORTAGAAGDPAMDW 90

RESULT 15
US-09-099-041A-10
Sequence 10; Application US/09099041A
Patent No. 6340576
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/99,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 10
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-09-099-041A-10

Query Match 17.1%; Score 64.5; DB 4; Length 100;
Best Local Similarity 28.6%; Pred. No. 0.5;
Matches 16; Conservative 12; Mismatches 19; Indels 9; Gaps 2;
2 LHFIDOHRAALIARYVNEMILDALYGVLTDEQYQAVERAEPTNPSKMRKL 52
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
6 IQLLKSNRELLVTHRNTQCLDNL--LKNDYFSAEAEIVCACPTOPDKVRKI 57

Search completed: July 28, 2004, 08:55:58
Job time : 12.4036 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:54:53 ; Search time 34.6446 Seconds

(without alignments)

642.856 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181

Perfect score: 378

Sequence: 1 GLHFIDQHRLAIIARVNTV.....LFSFTPANWTCKDILLQAL 71

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpa/US06_NEWPUB.pep:*

4: /cgn2_6/ptodata/1/pubpa/US06_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/1/pubpa/US08_NEWPUB.pep:*

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11: /cgn2_6/ptodata/1/pubpa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpa/US09_NEWPUB.pep:*

13: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpa/US10_NNEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpa/US09_NNEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpa/US09O_PUBCOMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	71	9 US-09-728-721-58	Sequence 58 , Appl
2	378	100.0	71	14 US-10-295-981-58	Sequence 58 , Appl
3	378	100.0	85	9 US-09-841-879B-8	Sequence 8 , Appl
4	378	100.0	85	16 US-10-756-097-8	Sequence 8 , Appl
5	378	100.0	90	9 US-09-931-071-7	Sequence 7 , Appl
6	378	100.0	195	9 US-09-728-721-49	Sequence 49 , Appl
7	378	100.0	195	9 US-09-996-617-8	Sequence 8 , Appl
8	378	100.0	195	9 US-09-941-879B-5	Sequence 5 , Appl
9	378	100.0	195	12 US-10-446-046-4	Sequence 4 , Appl
10	378	100.0	195	14 US-10-295-881-49	Sequence 55 , Appl
11	378	100.0	195	15 US-10-240-145-55	Sequence 84 , Appl
12	378	100.0	195	15 US-10-131-41-84	Sequence 541 , Appl
13	378	100.0	195	16 US-10-756-097-5	Sequence 541 , Appl
14	378	100.0	205	14 US-10-106-698-5421	Sequence 15 , Appl
15	269	71.2	85	16 US-10-756-097-15	Sequence 15 , Appl
17	264	69.8	70	9 US-09-728-721-57	Sequence 57 , Appl
18	264	69.8	70	14 US-10-295-981-57	Sequence 66 , Appl
19	264	69.8	70	14 US-10-295-981-66	Sequence 7 , Appl
20	264	69.8	84	9 US-09-841-879B-7	Sequence 7 , Appl
21	264	69.8	84	16 US-10-756-097-7	Sequence 61 , Appl
22	264	69.8	193	9 US-09-728-721-61	Sequence 2 , Appl
23	264	69.8	193	9 US-09-981-879B-2	Sequence 2 , Appl
24	264	69.8	193	14 US-10-295-981-61	Sequence 15 , Appl
25	264	69.8	193	14 US-10-295-981-61	Sequence 15 , Appl
26	264	69.8	193	16 US-10-756-097-2	Sequence 15 , Appl
27	216	57.1	88	9 US-09-841-739-15	Sequence 15 , App
28	216	57.1	88	14 US-10-449-31-15	Sequence 139 , App
29	216	57.1	442	10 US-09-895-298-139	Sequence 4 , Appl
30	216	57.1	1399	9 US-09-388-221-4	Sequence 2 , Appl
31	216	57.1	1429	9 US-09-931-071-2	Sequence 2 , Appl
32	216	57.1	1429	9 US-10-029-347-23	Sequence 3 , Appl
33	216	57.1	1429	12 US-10-029-347-26	Sequence 6 , Appl
34	216	57.1	1429	14 US-10-028-392-11	Sequence 11 , Appl
35	216	57.1	1429	14 US-10-028-374-3	Sequence 3 , Appl
36	216	57.1	1429	14 US-10-028-374-15	Sequence 15 , Appl
37	216	57.1	1429	14 US-10-183-770-3	Sequence 3 , Appl
38	216	57.1	1429	14 US-10-183-770-15	Sequence 15 , Appl
39	216	57.1	1429	14 US-10-938-221-6	Sequence 6 , Appl
40	216	57.1	1429	9 US-09-388-221-2	Sequence 2 , Appl
41	216	57.1	1473	9 US-09-388-221-2	Sequence 8 , Appl
42	216	57.1	1473	12 US-10-182-822A-8	Sequence 5422 , Ap
43	214	56.6	158	14 US-10-106-698-5422	Sequence 1120 , Ap
44	214	56.6	190	9 US-09-925-301-1120	Sequence 145 , Ap
45	141	37.3	65	10 US-09-895-298-145	Sequence 145 , Ap

ALIGNMENTS

RESULT 1
US-09-728-721-58
; Sequence 58 , Application US/09728721
; Patent No. US2010061845A1
; GENERAL INFORMATION:
; APPLICANT: Bartin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-1-2-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-58

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	71	9 US-09-728-721-58	Sequence 58 , Appl
2	378	100.0	71	14 US-10-295-981-58	Sequence 58 , Appl
3	378	100.0	85	9 US-09-841-879B-8	Sequence 8 , Appl
4	378	100.0	85	16 US-10-756-097-8	Sequence 8 , Appl
5	378	100.0	90	9 US-09-931-071-7	Sequence 7 , Appl
6	378	100.0	195	9 US-09-728-721-49	Sequence 49 , Appl
7	378	100.0	195	9 US-09-996-617-8	Sequence 8 , Appl
8	378	100.0	195	9 US-09-941-879B-5	Sequence 5 , Appl
9	378	100.0	195	12 US-10-446-046-4	Sequence 4 , Appl
10	378	100.0	195	14 US-10-295-881-49	Sequence 55 , Appl
11	378	100.0	195	15 US-10-240-145-55	Sequence 84 , Appl
12	378	100.0	195	15 US-10-131-41-84	Sequence 541 , Appl
13	378	100.0	195	16 US-10-756-097-5	Sequence 541 , Appl
14	378	100.0	205	14 US-10-106-698-5421	Sequence 15 , Appl
15	269	71.2	85	9 US-09-841-879B-15	Sequence 15 , Appl

Query Match 100.0%; Pred. No. 5.6e-40; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Mismatches 71; Conservative 0;
1 GLHFIDQHRAALIARVTNVILLELDALYKGKULTDQIQAVRAEPTNPDKMPLFSPTPAWN 60
QY Db 1 WTCDLILQLQI 71
1 GLHFIDQHRAALIARVTNVILLELDALYKGKULTDQIQAVRAEPTNPDKMPLFSPTPAWN 60
QY Db 61 WTCDLILQLQI 71
1 WTCDLILQLQI 71

RESULT 2
 US-10-295-981-58
 ; Sequence 58, Application US/10295981
 ; Publication No. US20030120055A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-124001
 ; CURRENT APPLICATION NUMBER: US/10/295, 981
 ; CURRENT FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US/09/340, 620
 ; PRIOR FILING DATE: 1999-06-28
 ; PRIOR APPLICATION NUMBER: US 09/245, 281
 ; PRIOR FILING DATE: 1999-02-05
 ; PRIOR APPLICATION NUMBER: US 09/207, 359
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 09/099, 041
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: US 09/019, 942
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 58
 ; LENGTH: 71
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-295-981-58

Query Match 100.0%; Score 378; DB 14; Length 71;
 Best Local Similarity 100.0%; Pred. No. 5.6e-40; Mismatches 0; Indels 0; Gaps 0;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAILIAARTNVWLLDALYGVLTDEQYQAVRAEPTNPNSKMRKLFSFTPWN 60
 Db 1 GLHFIDQHRAILIAARTNVWLLDALYGVLTDEQYQAVRAEPTNPNSKMRKLFSFTPWN 60

Qy 61 WTCKDILLQAL 71
 Db 61 WTCKDILLQAL 71

RESULT 3
 US-09-041-879B-8
 ; Sequence 8, Application US/09841879B
 ; Patent No. US20020142379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-330001
 ; CURRENT APPLICATION NUMBER: US/09/841, 879B
 ; CURRENT FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: US 09/728, 721
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: US 09/728, 721
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: US 09/728, 721
 ; PRIOR FILING DATE: 1999-06-28
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 85
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-041-879B-8

Query Match 100.0%; Score 378; DB 9; Length 85;
 Best Local Similarity 100.0%; Pred. No. 6.9e-40; Mismatches 0; Indels 0; Gaps 0;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAILIAARTNVWLLDALYGVLTDEQYQAVRAEPTNPNSKMRKLFSFTPWN 60
 Db 1 GLHFIDQHRAILIAARTNVWLLDALYGVLTDEQYQAVRAEPTNPNSKMRKLFSFTPWN 60

Qy 61 WTCKDILLQAL 71

RESULT 4
 US-10-756-097-8
 ; Sequence 8, Application US/10756097
 ; Publication No. US20040127655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-320001
 ; CURRENT APPLICATION NUMBER: US/10/756, 097
 ; CURRENT FILING DATE: 2004-01-13
 ; PRIOR APPLICATION NUMBER: US/09/841, 879B
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: US 09/728, 721
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: US 09/728, 721
 ; PRIOR FILING DATE: 1999-06-28
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 85
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-756-097-8

Query Match 100.0%; Score 378; DB 16; Length 85;
 Best Local Similarity 100.0%; Pred. No. 6.9e-40; Mismatches 0; Indels 0; Gaps 0;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAILIAARTNVWLLDALYGVLTDEQYQAVRAEPTNPNSKMRKLFSFTPWN 60
 Db 1 GLHFIDQHRAILIAARTNVWLLDALYGVLTDEQYQAVRAEPTNPNSKMRKLFSFTPWN 60

Qy 61 WTCKDILLQAL 71
 Db 61 WTCKDILLQAL 71

RESULT 5
 US-09-931-071-7
 ; Sequence 7, Application US/09931071
 ; Patent No. US20020128219A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; APPLICANT: Alnerri, Emad S.
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-335001
 ; CURRENT APPLICATION NUMBER: US/09/931, 071
 ; CURRENT FILING DATE: 2002-03-18
 ; PRIOR APPLICATION NUMBER: 09/428, 252
 ; PRIOR FILING DATE: 1999-10-27
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 7
 ; LENGTH: 90
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-931-071-7

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 Best Local Similarity 100.0%; Pred. No. 7.4e-40; Mismatches 0; Indels 0; Gaps 0;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 6 GLHFIDQHRAILIAARTNVWLLDALYGVLTDEQYQAVRAEPTNPNSKMRKLFSFTPWN 60

Qy 61 WTCKDILLQAL 71

RESULT 6
 US-09-728-721-49
 Sequence 49 Application US/09728721
 ; Patent No. US20020061845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-124 001
 ; CURRENT APPLICATION NUMBER: US/09/728,721
 ; CURRENT FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: 09/340,620
 ; PRIOR FILING DATE: 1999-06-28
 ; PRIOR APPLICATION NUMBER: US 09/207,359
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 09/099,041
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: US 09/019,942
 ; PRIOR FILING DATE: 1998-02-06
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 49
 ; LENGTH: 195
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-728-721-49

Query Match 100.0%; Score 378; DB 9; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.8e-39;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIARYTENVWILDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 60
 Db 111 GLHFIDQHRAALIARYTENVWILDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 170

Qy 61 WTCKDLILQL 71
 Db 171 WTCKDLILQL 181

RESULT 7
 US-09-996-617-8
 Sequence 8, Application US/0996617
 ; Patent No. US2002028198A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-140 001
 ; CURRENT APPLICATION NUMBER: US/09/996,617
 ; CURRENT FILING DATE: 2001-11-27
 ; PRIOR APPLICATION NUMBER: 09/931,071
 ; PRIOR FILING DATE: 2001-08-15
 ; PRIOR APPLICATION NUMBER: 09/428,252
 ; PRIOR FILING DATE: 1999-10-27
 ; PRIOR APPLICATION NUMBER: 09/340,620
 ; PRIOR FILING DATE: 1999-06-28
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 195
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-996-617-8

Query Match 100.0%; Score 378; DB 9; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.8e-39;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIARYTENVWILDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 60
 Db 111 GLHFIDQHRAALIARYTENVWILDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPWN 170

PRIOR FILING DATE: 1999-06-28
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5
 LENGTH: 195
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-755-097-5

Query Match Score 378; DB 16; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.8e-39; Indels 0; Gaps 0;
 Matches 71; Conservative 0; Mismatches 0; Other Information: xaa = Any Amino Acid
 US-09-841-879B-15

Qy 1 GLHFIDQHRAALIARYTVEWLIDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN 60
 Db 111 GLHFIDQHRAALIARYTVEWLIDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN 170

Qy 61 WTCKDILLQAL 71
 Db 171 WTCKDILLQAL 181

RESULT 14
 US-10-106-698-5421
 Sequence 5421, Application US/10106698
 Publication No. US20030109690A1

GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 FILE REFERENCE: PA0005P1
 CURRENT APPLICATION NUMBER: US/10/106,698
 CURRENT FILING DATE: 2004-03-27
 PRIOR APPLICATION NUMBER: PCT/US00/26524
 PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: US 60/157,137
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: US 60/163,280
 PRIOR FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: PatentIn Ver. 3.0
 SEQ ID NO: 5421
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-106-698-5421

Query Match Score 378; DB 14; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.9e-39; Indels 0; Gaps 0;
 Matches 71; Conservative 0; Mismatches 0; Other Information: xaa = Any Amino Acid
 US-09-841-879B-15

Qy 1 GLHFIDQHRAALIARYTVEWLIDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN 60
 Db 121 GLHFIDQHRAALIARYTVEWLIDALYGRVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN 180

Qy 61 WTCKDILLQAL 71
 Db 181 WTCKDILLQAL 191

RESULT 15
 US-09-841-879B-15
 Sequence 15, Application US/09841879B
 Patent No. US20020142379A1
 GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
 FILE REFERENCE: 07334-330001
 CURRENT APPLICATION NUMBER: US/09/841,879B
 CURRENT FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: US 09/728,721
 PRIOR FILING DATE: 2000-12-01
 PRIOR APPLICATION NUMBER: US 09/340,620
 PRIOR FILING DATE: 1999-06-28



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665.325 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181

Perfect score: 378

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Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : PIR:78;*

1: Pi1=;*

2: pi2=;*

3: pi3=;*

4: pi4=;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	216	57.1	1192	2	T17255	hypothetical prote
2	69.8	18.4	221	2	S70009	glutamate/proline-
3	68	18.0	545	2	A87136	hypothetical prote
4	64.5	17.1	605	2	T04197	hypothetical prote
5	64	16.9	304	2	G81417	cytochrome-c perox
6	62.5	16.5	211	2	S57940	Yggd protein homolog
7	62	16.4	779	2	AB2402	alpha-glucosidase
8	61.5	16.3	306	2	T21132	hypothetical prote
9	61	16.3	346	2	A48470	translation elonga
10	61.5	16.3	1193	2	T21133	hypothetical prote
11	61	16.1	338	2	AF0294	probable lipate-P
12	61	16.1	345	2	T17608	probable GDPmannos
13	61	16.1	464	2	H82011	probable outer mem
14	60.5	16.0	724	2	C71274	hypothetical prote
15	60.5	16.0	877	2	JN0772	glucan endo-1,3-be
16	60.5	16.0	332	2	C83295	conserved hypoth
17	60	15.9	773	2	T39513	hypothetical prote
18	60	15.9	249	2	A35263	beta-lactamase (EC
19	59.5	15.7	290	2	I58425	arylamine N-acetyl
20	59	15.6	286	2	B82201	sphingidine/pitresc
21	59	15.6	371	2	S68072	major outer membra
22	59	15.6	381	2	B88427	protein R0735.3 [i
23	59	15.6	529	2	S43599	Snf5 homolog R07B5
24	59	15.6	537	2	S62749	A-alpha X protein
25	59	15.6	542	2	D70873	probable ABC trans
26	59	15.6	681	2	B70942	hypothetical prote
27	59	15.6	1021	2	S09111	hypothetical prote
28	59	15.6	1023	2	G96509	protein F27E5.21 [
29	59	15.6	233	2	S62063	

ALIGNMENTS

RESULT 1						
T17255	hypothetical protein DKFPz586Q1822.1 - human (fragment)					
C;Species: Homo sapiens (man)						
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 15-Oct-1999						
C;Accession: T17255						
R;Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.						
Submitted to the Protein Sequence Database, September 1999						
A;Reference number: Z18722						
A;Accession: T17255						
A;Status: preliminary						
A;Molecule type: mRNA						
A;Residues: 1-1192 <KO>						
A;Cross-references: EMBL:AL117470						
A;Experimental source: adult uterus; c1one DKFPz586Q1822						
C;Genetics:						
A;Note: DKFPz586Q1822.1						
Query	2 LHFIDQHRAALIARYVNVEWLLDIALYKVLDEQYQAVRAEPTNPNSKMRKLFSFTPAWNW 61	Match	57.1%	Score	216	DB 2; Length 1192;
Best Local Similarity	61.4%	Pred. No.	6.1e-17;			
Matches	43;	Conservative	12;	Mismatches	15;	Indels 0; Gaps 0;
Qy	1098 LHFVDQRBQLIARYVNVEWLLDIALYKVLDEQYQAVRAEPTNPNSKMRKLFSFTPAWNW 61	Db				
Qy	62 TCKDLIQL 71	Db				
Db	1158 KCKDGLYQAL 1167					
RESULT 2						
S70009	glutamate/proline-rich protein (clone 53.1.1.1) - rat					
C;Species: Rattus norvegicus (Norway rat)						
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999						
C;Accession: S70009						
R;Geerman, R.; McMahon, A.; Sabban, B.L.						
Biochim. Biophys. Acta 1306, 147-152, 1996						
A;Title: Cloning and characterization of cDNAs for novel proteins with glutamic acid-pr						
A;Reference number: S70005; PMID:96221285; PMID:8834331						
A;Accession: S70009						
A;Status: preliminary						
A;Molecule type: mRNA						
A;Residues: 1-221 <GEB>						
A;Cross-references: EMBL:U406227; NID:91184693; PID:91184694						
Query	18.4% Score 69.5; DB 2; Length 221;	Match				
Best Local Similarity	26.8%; Pred. No. 1.3;	Mismatches	22;	Conservative	12;	Mismatches 23; Indels 25; Gaps 3;
Qy	5 IDQHRAALIARYVNVEWLLDIALYKVLDEQYQAVRAEPTNPNSKMRKLFSFT----- 56	Db				

R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takizawa, M.; Yamada, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120; Reference number: AB1807; PMID:11759840
A; Accession: AE2402
A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: GB:PA000019; PIDN:BAB76472.1; PMID:917133910; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: air4773

RESULT 8
T21132 hypothetical protein F20B10.2 - Caenorhabditis elegans

Query Match Score 16.4%; DB 2; Length 779;
Best Local Similarity 35.7%; Pred. No. 41;
Matches 15; Conservative 6; Mismatches 13; Indels 8; Gaps 2;
R; Percy, C.
Qy 6 DQH----RAALIARVNIV--EMLLDALYGRVLTDEQYAV 39
Db 141 DEHFYFGBERTGLDQIATIRTNWACDALDYDVLTDNMYQAI 182

RESULT 8
T21132 hypothetical protein F20B10.2 - Caenorhabditis elegans

C; Species: Caenorhabditis elegans
C; Accession: T21132
R; Percy, C.
Submitted to the EMBL Data Library, February 1996
A; Reference number: Z21380
A; Accession: T21132
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-306 <WIL>
A; Cross-references: EMBL:Z69636; PIDN:CAA93464.1; GSPDB:GN00022; CESP:F20B10.2
A; Experimental source: clone F20B10
C; Genetics:
A; Map Position: 4
A; Gene: CBS:P:F20B10.2
A; Introns: 18/1; 74/3; 135/1; 222/3; 258/3; 279/1

Query Match Score 61.5%; DB 2; Length 306;
Best Local Similarity 34.0%; Pred. No. 17;
Matches 10; Mismatches 20; Indels 3; Gaps 2;

Qy 13 IARYT--NVEENLDALYGRV-LTDEQYQAVRAEPPNPSKVRKLFSFTPAW 59
Db 37 LKRVTTRLSVSGHSAYHVKSISDDFQLVRLSNPVLVYSTLSNTPSW 86

RESULT 11

F83616 hypothetical protein PA0234 [imported] - Pseudomonas aeruginosa (strain PA01)

C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: F83616
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Baldwin, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A; Reference number: A82950; PMID:20437337; PMID:10984043
A; Accession: F83616
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-277 <SPO>
A; Cross-references: GB:AE004461; GB:AE004091; NID:99946066; PIDN:AGG03623.1; GSPDB:GN001

A; Experimental source: strain PA01
C; Genetics:
A; Gene: PA0234

RESULT 9

A4870 translation elongation factor eEF-1 alpha chain - *Eimeria bovis* (fragment)
C; Species: *Eimeria bovis*
C; Date: 01-Dec-1993 #sequence_revision 15-Oct-1994 #text_change 12-Apr-1995
C; Accession: A48470
R; Abrahamsen, M.S.; Clark, T.G.; Mascolo, P.; Speer, C.A.; White, M.W.
Mol. Biochem. Parasitol. 57, 1-14, 1993
A; Title: Developmental gene expression in *Eimeria bovis*.
A; Reference number: A48470; PMID:93149194; PMID:8426605
A; Accession: A48470
A; Molecule type: mRNA
A; Residues: 1-346 <ABR>
A; Experimental source: merozoites
A; Note: sequence extracted from NCBI backbone (NCBIN:123619, NCBIPI:123622)
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C; Keywords: GTP binding; protein biosynthesis

Query Match Score 16.3%; DB 2; Length 346;
Best Local Similarity 21.7%; Pred. No. 19;
Matches 15; Conservative 13; Mismatches 34; Indels 7; Gaps 1;

Qy 5 IDQHRAALIARVNIVEWLIDALYGRVLTDEQYQAVRAEPTNPSKVRKLFSFTPAW 57
Db 246 VDCHTAIACKFAVILEKRLDRSGTALEDDPFKTFITGDAATIKMPEPKPMCVSESSIEYPP 305
Qy 58 AWNTWCKDL 66
Db 306 LGRAFVRDM 314

RESULT 10
T21133 hypothetical protein F20B10.1 - Caenorhabditis elegans

C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T21133
R; Percy, C.
Submitted to the EMBL Data Library, February 1996
A; Reference number: Z19380
A; Accession: T21133
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-193 <WIL>
A; Cross-references: EMBL:Z69636; PIDN:CAA93465.1; GSPDB:GN00022; CESSP:F20B10.1
A; Experimental source: clone F20B10
C; Genetics:
A; Gene: CBS:P:F20B10.1
A; Map Position: 4
A; Introns: 18/1; 74/3; 135/1; 222/3; 258/3; 279/1; 379/1; 496/1; 791/2; 867/1; 969/1; 1

Query Match Score 16.3%; DB 2; Length 1193;

Best Local Similarity 34.0%; Pred. No. 76;
Matches 17; Conservative 10; Mismatches 20; Indels 3; Gaps 2;
A; Gene: F20B10.1
A; Map Position: 4
A; Introns: 18/1; 74/3; 135/1; 222/3; 258/3; 279/1; 379/1; 496/1; 791/2; 867/1; 969/1; 1

Query Match Score 61.5%; DB 2; Length 1193;
Best Local Similarity 34.0%; Pred. No. 76;
Matches 17; Conservative 10; Mismatches 20; Indels 3; Gaps 2;

Qy 13 IART--NVEENLDALYGRV-LTDEQYQAVRAEPPNPSKVRKLFSFTPAW 59
Db 37 LKRVTTRLSVSGHSAYHVKSISDDFQLVRLSNPVLVYSTLSNTPSW 86

RESULT 11

F83616 hypothetical protein PA0234 [imported] - Pseudomonas aeruginosa (strain PA01)

C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: F83616
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Baldwin, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A; Reference number: A82950; PMID:20437337; PMID:10984043
A; Accession: F83616
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-277 <SPO>
A; Cross-references: GB:AE004461; GB:AE004091; NID:99946066; PIDN:AGG03623.1; GSPDB:GN001

A; Experimental source: strain PA01
C; Genetics:
A; Gene: PA0234

Query Match Score 16.1%; DB 2; Length 277;

Best Local Similarity 32.8%; Pred. No. 17;
Matches 20; Conservative 11; Mismatches 12; Indels 18; Gaps 4;
Qy 7 QHRALIARY----TNVENVLLDAI---YGRVLTDEQYQAVRAEPTNPSKVRKLFSFTPAW 57
Db 6 QSAALIALVGAGESMALEWMSNVGFRYQQFTN-----PNNPDPKFKRYSFTH 56

Qy 58 A 58
Db 57 A 57

RESULT 12
 AF0294 probable lipoate-protein ligase A lpla [imported] - Yersinia pestis (strain C092)
 C;Species: Yersinia pestis
 C;Accession: AF0294 Sequence revision 02-Nov-2001 #text_change 09-Nov-2001
 R;Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davis, R.M.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001.
 A;Title: Genome sequence of Yersinia Pestis, the causative agent of plague.
 A;Reference number: AB0001; M0ID:21470413; PMID:11586360
 A;Accession: AF0294
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-38 <RTR>
 A;Cross-references: GB:AL590842; PIDN:GAC91218.1; PID:gi15980407; GSPDB:GN00175
 C;Genetics:
 A;Gene: lpla
 C;Superfamily: lipoate-protein ligase

Query Match	Score 61;	DB 2;	Length 336;
Best Local Similarity	16.1%;	Pred. No. 21;	
Matches	32.3%;	Indels	20;
Qy	14 ARVNTVWLLDAL-YKVLT-----DEQ?OAVREPTNSKMRKLFSFT-----56	Gaps	4;
Db	183 SRVTNLVLLPGIDHGKIRTAIEQAFFAYDEQ---VSAEVISPOSLLPGLFTEQFAQKQ		239

RESULT 15
 C71274 hypothetical protein TP0851 - syphilis spirochete
 C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Nov-1999
 C;Accession: C71274
 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwirtzman, J.; Khailak, H.; Richardson, D.; Howell, J.; Chidambaram, M.; Utterback, T.; McDaniel, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998.
 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A;Reference number: A71250; PMID:98332770; PID:965876
 A;Accession: C71274
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-724 <COL>
 A;Cross-references: GB:AP001255; GB:AE000520; PID:gi3323156
 A;Experimental source: strain Nichols
 C;Genetics:
 A;Gene: TP0851
 C;Superfamily: syphilis spirochete hypothetical protein TP0851

RESULT 13
 TI7608 probable GDPmannose 4,6-dehydratase (EC 4.2.1.47) - Chlorella virus PBCV-1
 N;Alternate names: GDP-D-mannose dehydratase
 C;Species: Chlorella virus PBCV-1
 C;Accession: TI7608 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: TI7608
 R;Graves, M.V.; van Etten, J.L.
 Submitted to the EMBL Data Library, May 1999
 A;Reference number: Z18806
 A;Accession: TI7608
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-345 <GRNA>
 A;Cross-references: EMBL:042550; PID:gi02886; PIDN: AAC96486.1
 C;Genetics:
 A;Note: A18R
 C;Superfamily: GDP-D-mannose dehydratase
 C;Keywords: carbon-oxygen lyase; hydro-lase

Query Match	Score 61;	DB 2;	Length 345;
Best Local Similarity	16.1%;	Pred. No. 22;	
Matches	28.6%;	Indels	24;
Qy	8 HRAALIARV--TNVNLDA-----LYGKVLTDEQYQAVRAEPTNFSK 48	Gaps	3;
Db	91 HOAEVTANVDALGVRLLDIAVRAGLNSRICQASITSELLGKVQEIPQERTPFYPRSPYX		150

RESULT 14
 H82011 probable outer membrane protein NMA0178 [imported] - Neisseria meningitidis (strain 2249)
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

Search completed: July 28, 2004, 08:55:21
 Job time : 12.2651 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:37 ; Search time 6.84337 Seconds
(without alignments)

Sequence: US-09-996-617-8_COPY_111_181
1 GLHFIDOHRLAIIARVTNVE.....LFSPTPAWNWTCKDILLQAL 71

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SwissProt_42:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	378	100.0	195	1	ASC_HUMAN	Q9ulz3 homo sapien
2	264	69.8	193	1	ASC_MOUSE	Q9pb4 mus musculu
3	216	57.1	1473	1	NALI_HUMAN	Q9g000 homo sapien
4	106	28.0	203	1	ASC_BRAKE	Q919n6 brachydano
5	69.5	18.4	219	1	NOL3_HUMAN	Q6936 homo sapien
6	69.5	18.4	220	1	NOL3_MOUSE	Q9d1x0 mus musculu
7	69.5	18.4	221	1	NOL3_RAT	Q62881 rattus norv
8	68.5	18.1	431	1	CAR8_HUMAN	Q9v292 homo sapien
9	67.5	17.9	539	1	RIK2_MOUSE	P51801 mus musculu
10	66.5	17.6	611	1	BIR1_CHICK	Q9k660 gallus gallu
11	65	17.2	598	1	DX52_MOUSE	Q8k101 mus musculu
12	64.5	17.1	953	1	CAR4_HUMAN	Q9r239 homo sapien
13	62.5	16.5	540	1	YGGA_AERHY	P55047 aeromonas h
14	62.5	16.5	540	1	RIK2_HUMAN	Q43353 receptor-
15	62	16.4	598	1	DX52_RAT	Q9bpt0 rattus norv
16	61.5	16.3	346	1	EPLA_EIMBO	P00751 eimeria bov
17	60.5	16.0	724	1	Y511_TREPA	Q9dpb3 treponema p
18	60	15.9	259	1	LP15_HUMAN	Q8r9ch9 mus musculu
19	60	15.9	332	1	DUSA_PSEAI	Q9j048 pseudomonas
20	60	15.9	332	1	DUSA_PSEAI	P79384 gallus galli
21	60	15.9	494	1	ENP2_CHICK	P22910 bacteroides
22	59.5	15.7	249	1	BLAB_BACFR	P55298 rattus norv
23	59.5	15.7	290	1	ARY2_RAT	P4027 haemophilus
24	59.5	15.7	347	1	HSLO_STRP3	P16425 drosophila
25	59	15.6	290	1	OB25_HAETIN	P52935 mus musculu
26	59	15.6	371	1	Y2R2_DROME	Q8bb9 streptococc
27	59	15.6	1021	1	ARY2_MOUSE	P4027 haemophilus
28	58.5	15.5	290	1	BIR2_MOUSE	P16425 drosophila
29	58.5	15.5	612	1	CAR4_MOUSE	P52935 mus musculu
30	58	15.5	953	1	SP21_BACSH	Q8bb9 mus musculu
31	58	15.3	117	1	ARY1_RAT	Q32223 bacillus sp
32	57.5	15.2	290	1	PR3B_HUMAN	P50297 rattus norv
33	57.5	15.2	350	1	LSS1_MOUSE	P22945 mus musculu

ALIGNMENTS

RESULT 1	
ASC_HUMAN	STANDARD; PRT; 195 AA.
ID	Q9ULZ3; Q96D12; Q9BS55; Q9HBDO; Q9NJK8;
AC	Q9ULZ3; Q96D12; Q9BS55; Q9HBDO; Q9NJK8;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Apoptosis-associated speck-like protein containing a CARD (hASC)
DE	(PYCARD) (Target of methylation-induced silencing 1) (Caspase recruitment domain protein 5).
GN	ASC OR TMS1 OR CARD5.
OS	Homo sapiens (Human)
OC	Bukarotai; Metacrocis; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
RN	[1]
SEQUENCE FROM N.A. (ISOFORM 1).	
RX	TISSUE-Leukemia; MEDLINE=20036508; PubMed=10567338; NCBITaxID=9606;
RC	NCBI_TaxID=9606;
RT	SEQUENCE FROM N.A. (ISOFORM 1).
RN	[2]
RA	Masumoto J., Taniguchi S., Aynukawa K., Sarvorham H., Kishino T., Nikawa N., Hidaka E., Matsuyama T., Higuchi T., Sagara J., "ASC, a novel 22-kDa protein, aggregates during apoptosis of promyelocytic leukemia HL-60 cells.", J. Biol. Chem. 274:38385-38388(1999).
RP	SEQUENCE FROM N.A. (ISOFORM 1 AND 2).
RC	TISSUE-Fibroblast; MEDLINE=1052139; PubMed=11103776;
RT	"ASC, a novel proapoptotic caspase recruitment domain protein that targets methylation-induced gene silencing in human breast cancers.", Cancer Res. 60:6236-6242(2000).
RN	[3]
RA	Martinon F., Hofmann K., Tschopp J., "PyCARD and CARD-containing molecule.", Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RC	TISSUE-Colon mucosa; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RT	"CARDs protein is a CARD/PYRIN family member that is involved in apoptotic signal transduction.", Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN	[4]
RA	Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T., Suzuki Y., Obayashi N., Nishi T., Shibanbara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEPD human cDNA sequencing project.", Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RC	TISSUE-Colon mucosa; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RT	"CARDs protein is a CARD/PYRIN family member that is involved in apoptotic signal transduction.", Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN	[5]
RA	Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T., Suzuki Y., Obayashi N., Nishi T., Shibanbara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEPD human cDNA sequencing project.", Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RC	TISSUE-Colon mucosa; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RT	"CARDs protein is a CARD/PYRIN family member that is involved in apoptotic signal transduction.", Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN	[6]
RA	Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T., Suzuki Y., Obayashi N., Nishi T., Shibanbara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEPD human cDNA sequencing project.", Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A. (ISOFORM 1 AND 3).
RC	TISSUE-Lymph, and Pancreas;

RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	FT DOMAIN 105 193 CARD.
RA	Blackie J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,	FT CONFLICT 159 159 K -> E (IN REF. 3).
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gruboldi M.,	FT SEQUENCE 193 AA; 21458 MW; 2A4EA40194870B31 CRC64;
RA	Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,	SQ
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombara P.,	Query Match 69.8%; Score 264.
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,	RT Best local Similarity 73.9%; Pred. NO. 7/re-24;
RA	Sasaki H., Sato K., Schoenbach C., Soya T., Shibata Y., Storch K.-P.,	CC Matches 51; Conservative 73.9%; Mismatches 11; Indels 0; Gaps 0;
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,	RT
RA	Hayashizaki Y., Functional annotation of a full-length mouse cDNA collection.;	RT
RL	Nature 409:85-90(2000).	RL
RN	SEQUENCE FROM N.A.	RN
RX	MEDLINE:22388257; PubMed=12477932;	RX
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	RA
RA	Altschul S.F., Collins F.S., Wagner L., Max S.I., Wang J., Hsieh F.,	RA
RA	Klausner R.D., Collier N.J., Farmer A.A., Rubin G.M., Hong L.,	RA
RA	Diacharenko L., Marusina K., Farmer D., Schaefer C.F., Bhat N.K.,	RA
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RA
RA	Stapleton M., Soares M.B., Bonaldo M.F., Rubin G.M., Hong L.,	RA
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.B.,	RA
RA	Raha S.S., Loquaiola N.A., Carninci P., Prange C.,	RA
RA	Bosak S.A., McEwan P.J., Abramson R.D., Mullally S.J.,	RA
RA	Richardson S., Worley K.C., Hale A.M., Garcia P.J., Malek J.A., Gunnarsson P.H.,	RA
RA	Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RA
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	RA
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	RA
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA
RA	Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M.,	RA
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,	RA
RT	"G"eneration and initial analysis of more than 15,000 full-length	RT
RT	human and mouse cDNA sequences.;	RT
RL	Proc. Natl. Acad. Sci. U.S.A. 99:11689-11693(2002).	RL
CC	-!- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic	CC
CC	activity is mediated predominantly through the activation of	CC
CC	caspase 9 (By similarity).	CC
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,	CC
CC	a redistribution from the cytoplasm to the aggregates occurs.	CC
CC	These appeared as hollow, perinuclear spherical, ball-like	CC
CC	structures (By similarity).	CC
CC	-!- TISSUE SPECIFICITY: Expressed in small intestine, colon, thymus,	CC
CC	spleen, brain, heart, skeletal muscle, kidney, lung and liver.	CC
CC	-!- DEVELOPMENTAL STAGE: Strongly expressed at E9.5 day in the	CC
CC	telencephalon, thalamic areas of the diencephalon, heart and	CC
CC	liver.	CC
CC	-!- SIMILARITY: Contains 1 CARD domain.	CC
CC	-!- SIMILARITY: Contains 1 CARD domain.	CC
CC	-----	CC
DR	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	CC
CC	the European Bioinformatics Institute. There are no restrictions on its	CC
CC	use by non-profit institutions as long as its content is in no way	CC
CC	modified and this statement is not removed. "Usage by and for commercial	CC
CC	entities requires a license or agreement (See http://www.ish-sib.ch/announce/ or send an email to license@ish-sib.ch).	CC
CC	-----	CC
DR	EMBL: AB032249; BAB16609_1;	DR
DR	EMBL: AF310104; AAG30387_1; -;	DR
DR	EMBL: AK003852; BAB26543_1; -;	DR
DR	EMBL: AK007742; BAB25229_1; -;	DR
DR	EMBL: AK016682; BAB31441_1; -;	DR
DR	EMBL: BC002522; AAB08352_1; -;	DR
DR	MGD: MGI:1931465; ASC	DR
DR	GO:0005829; C:cytosol; IDA.	DR
DR	InterPro: IPR001315; CARD.	DR
DR	InterPro: IPR0004020; PAAD_DAPIN_dom.	DR
DR	Pfam: PF02158; PAAD_DAPIN_1.	DR
DR	PROSITE: PS50209; CARD_1.	DR
DR	PROSITE: PS50824; DAPIN_1.	DR
XW	Apoptosis; Anti-oncogene.	XW
FT	-----	FT

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CC EMBL; AP21013; AAF6956..1.;

CC DR ZFIN; ZDB-GENE-005511-2; asc1.

CC DR InterPro; IPR001315; CARD.

CC DR InterPro; IPR004020; PAAD-DAPIN_dom.

CC DR Pfam; PF05758; PAAD_DAPIN; 1.

CC DR PROSITE; PSS0209; CARD.

CC DR PROSITE; PSS0824; DAPIN; 1.

CC KW Apoptosis; Anti-oncogene.

FT DOMAIN 1 91 DAPIN.

FT DOMAIN 112 203 CARD.

SEQUENCE 203 AA; 22867 MW; EF57179EB7A7 CRC64;

Query Match 2 LHFIDORRAALIARYTNVWILDAL-YGRVLTDQYQAATRFPNPSKXPKLFS--FPFA 58

Best Local Similarity 42.5%; Pred. No. 3e-05; Matches 13; Mismatches 25; Indels 4; Gaps 3;

Matches 31; Conservative 13; Name=1; Synonyms=Myp;

Db 117 VNFIDDHKEELIDRNVNDPLDLRQKVITNEYCIRTRKEIPEQKMRRELLTGPICA 176

Query 59 WNWTKDILQLQAL 71

Db 177 GN-KGKREVLDAL 188

RESULT 5

NOL3_HUMAN STANDARD; PRT; 219 AA.

ID NOL3_HUMAN STANDARD; PRT; 219 AA.

AC 069316; 060937; STANDARD; PRT; 219 AA.

DE cytoplasmic protein (Myp) (Nucleolar protein of 30 kDa) (Nop30).

DT 28-FEB-2003 (Rel. 41; Created)

DT 28-FEB-2003 (Rel. 41; Last annotation update)

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DE Nucleolar protein 3 (Apoptosis repressor with CARD) (Muscle-enriched DE

cytoplasmic protein (Myp) (Nucleolar protein of 30 kDa) (Nop30).

GN NOL3 OR ARC OR NOP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TAXID=9606; OX [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=98226784; PubMed=9560245;

RA Koseki T., Inohara N., Chen S., Nunez G.;

RT "ARC, an inhibitor of apoptosis expressed in skeletal muscle and heart

that interacts selectively with caspases.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:5156-5160(1998).

RC TISSUE=Cervical carcinoma

RX MEDLINE=99214168; PubMed=10196175;

RA Stoss O., Schwaiger F.-W., Cooper T.A., Stamm S.;

RT "Alternative splicing determines the intracellular localization of the novel nuclear protein Nop30 and its interaction with the splicing

factor SRP30c.";

RL J. Biol. Chem. 274:10951-10962(1999).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Kidney

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Brat N.K.,

Hopkins R.P., Jordan A., Moore T., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marsina K., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Orange C.,

Raha S.S., Loqueilano N.A., Peters G.J., Abramson R.D., Mullally S.J.,

Bosak S.A., McEwan P.J., McFernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madar A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schein J.B., Jones S.J.M., Marrs M.A., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnarch A., Schein J.B., Jones S.J.M., Marrs M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: The nuclear isoform (1/Nop10) may be involved in RNA splicing and the cytoplasmic isoform (2/Myp) may inhibit apoptosis.

CC -1- SUBUNIT: Isoform 1 oligomerizes and binds to SFR9/SRP30C and also interacts with NPM1. Isoform 2 binds caspase-2, caspase-8 and CED-3 and inhibits caspase-8 activity.

CC -1- SUBCELLULAR LOCATION: Nuclear or cytoplasmic. Isoform 1 is found in nucleoli and nucleoplasm. Isoform 2 is cytoplasmic.

CC -1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Isoid=060336-1; Sequence=Displayed;

Name=1; Synonyms=Myp;

Name=2; Synonyms=Nop30;

CC -1- TISSUE SPECIFICITY: Highly expressed in heart and skeletal muscle.

CC -1- Detected at low levels in placenta, liver, kidney and pancreas.

CC -1- SIMILARITY: Contains 1 CARD domain.

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CC DR AF064599; AAC18593..1;

CC DR AF064600; AAC18594..1;

CC DR AF064598; AAC18590..1;

CC DR AF064597; AAC18591..1;

CC DR AF043244; AAC14993..1;

CC DR EMBL; BC012798; AAH12798..1;

CC DR Genew; HGNC:7869; NOL3..

CC DR GR; O61936; ..

CC DR MM; 605235; ..

CC DR InterPro; IPR001315; CARD.

CC SMART; SM00114; CARD; 1.

CC DR PROSITE; P50209; CARD; 1.

CC FT DOMAIN 4 95 Apoptosis; Nuclear protein; mRNA splicing; CARD.

CC FT VARSPLIC 96 219 RAPRPNPGPERSSWSKURPLKLNRSSRSQSQSNPRK

CC FT G-> VGGTGRDRSDPPSRKGTSQPSPTCRPAPGSGTCPLPRAS

CC FT DPDEAGCGEGSEBAVGSTPZPRPEPELEAEASKEAPEPEPE

CC FT PELEPELAABEPEPELEPEPELEPEPEDESEDS (in

CC Isoform 2).

CC FT ID=VSP_000789; /FTID=VSP_000789;

CC SQ SEQUENCE 219 AA; 24327 MW; B1CCCB13D4FEE09 CRC64;

CC Query Match 18.4%; Score 69.5; DB 1; Length 219;

CC Best Local Similarity 26.8%; Pred. No. 0.63;

CC Matches 22; Conservative 12; Mismatches 23; Indels 25;

CC Gaps 3;

Qy 5 TDQRHIALIAY-TNYENLILDALYGR-VLTDQYQAVRAFBPTNPSKMRKLFST-----

Db 12 IDREKRKLVTIQLQDSLGLDALLARGVLTPEYEALDADPAERVRRLLLVQKGGEA 71

Qy 57 -----PANNW 61

Db 72 ACQELLRCQRTAGAPDPDW 93

RN [2]	SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.	DR DR Pfam; PF00619; CARD; 1.
RP TISSUE=Breast;		DR DR Pfam; PF05729; NACHT; 1.
RC MEDLINE=99162599; PubMed=10325646;		DR DR PROSITE; PS50209; CARD; 1.
RX Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio R.,		DR DR PROSITE; PS50837; NACHT; 1.
RA Merino J., Liu D., Ni J., Nunez G.,		KW KW Apoptosis; ATP-binding; Repeat; Leucine-rich repeat.
RT kappaB"; an Apaf-1-like activator of caspase-9 and nuclear factor-		CARD.
RT kappaB";		FT FT DOMAIN 196 105
J. Biol. Chem. 274:14560-14567(1999).		FT FT DOMAIN 196 531
RN [3]	SEQUENCE FROM N.A.	FT FT NP-BIND 202 209
RP TISSUE=Lymph;		FT FT REPEAT 632 656
RX MEDLINE=22388257; PubMed=12477932;		FT FT REPEAT 702 725
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		FT FT REPEAT 702 750
RA Klaesner R.D., Collens F.S., Wagner L., Sheinman C.M., Schuler G.D.,		FT FT REPEAT 727 750
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		FT FT REPEAT 755 778
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		FT FT REPEAT 783 806
RA Diatchenko L., Marusina K., Farmer J., Rubin G.M., Hong L.,		FT FT REPEAT 839 862
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		FT FT REPEAT 867 891
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		FT FT REPEAT 895 918
RA Rosa S.A., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		FT FT REPEAT 923 946
RA Bosak S.A., McEvani P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		FT FT MUTAGEN 41 41
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		FT FT MUTAGEN 41 41
RA Villanueva D.K., Muzny D.M., Sodargran E.J., Lu X., Gibbs R.A.,		FT FT MUTAGEN 41 41
RA Fahey J., Helton E., Kettman J., Madan A., Rodin J., Sanchez A.,		FT FT MUTAGEN 41 41
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		FT FT MUTAGEN 41 41
RA Blakesley R.W., Grimes J.W., Green E.D., Dickson M.C.,		FT FT MUTAGEN 41 41
RA Rodriguez A.C., Touchman J.W., Schmutz J., Myers R.M.,		FT FT MUTAGEN 41 41
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,		FT FT MUTAGEN 41 41
RA Scherich A., Schein J.B., Jones S.J.M., Marra M.A.,		FT FT MUTAGEN 41 41
RT "Generation and initial analysis of more than 15,000 full-length		FT FT MUTAGEN 41 41
RT human and mouse cDNA sequences";		FT FT MUTAGEN 41 41
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		FT FT MUTAGEN 41 41
RN [4]	FUNCTION.	FT FT PRT; 225 AA.
RP MEDLINE=21264704; PubMed=11058605;		FT FT PRT; 225 AA.
RA Inohara N., Ogura Y., Chen F.F., Moto A., Nunez G.;		FT FT PRT; 225 AA.
RT "Human Nod1 confers responsiveness to bacterial lipopolysaccharides.";		FT FT PRT; 225 AA.
RL J. Biol. Chem. 276:2551-2554(2001).		FT FT PRT; 225 AA.
CC -!- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-B activity via RICK (CARDIAK, RIP2) and Ikk-gamma. Contains repeats to intracellular bacterial lipopolysaccharides (LPS).		FT FT PRT; 225 AA.
CC -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD interaction.		FT FT PRT; 225 AA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.		FT FT PRT; 225 AA.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal muscle, pancreas, spleen and ovary. Also detected in placenta, lung, liver, kidney, thymus, testis, small intestine and colon.		FT FT PRT; 225 AA.
CC -!- SIMILARITY: Contains 1 CARD domain.		FT FT PRT; 225 AA.
CC -!- SIMILARITY: Contains 1 NACHT domain.		FT FT PRT; 225 AA.
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.		FT FT PRT; 225 AA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		FT FT PRT; 225 AA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		FT FT PRT; 225 AA.
DR EMBL; AF126484; AAD29125; 1;		CC -!- SUBCELLULAR LOCATION: BELONGS TO THE LYSEYGBA FAMILY.
DR EMBL; AF149774; AAD43922; 1;		CC -!- SIMILARITY: BELONGS TO THE LYSEYGBA FAMILY.
DR EMBL; AF13925; AAD28350; 1;		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR Genew; HGNC:16390; CARD4.		CC DR EMBL; X89469; CA6165; 1; ALT INIT.
DR NM_001980; -;		DR InterPro; IPR00477; LYSE exporter.
DR GO; GO:0008656; F: caspase activator activity; TAS.		DR InterPro; IPR01123; LYSE.
DR GO; GO:0006915; P: apoptosis; TAS.		DR Pfam; PF01810; LYSE.
DR GO; GO:0007165; P: signal transduction; TAS.		DR TIGRFAMS; TIGR00948; 2a75; 1.
DR InterPro; IPR007915; CARD.		KW KW Hypothetical protein/Transmembrane.
DR InterPro; IPR00791; LRR_Rninh.		FT TRANSMEM 1 21 POTENTIAL.
DR InterPro; IPR00711; NACHT_NTPase.		FT TRANSMEM 37 57

FT	TRANSMEM	65	85	POTENTIAL.	RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
FT	TRANSMEM	116	136	POTENTIAL.	RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
FT	TRANSMEM	150	170	POTENTIAL.	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
SQ	SEQUENCE	225 AA;	24482 MW;	172DB104473B0B9 CRC64;	RA	Raha S.S., Lonquihua N.R., Peters G.J., Abramson R.D., Mulahay S.J.,
Query Match		16.5%	Score 62.5%; DB 1; Length 225;	RA	Bosak S.A., McElvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
Best Local Similarity		24.6%	Pred. No. 4.3%;	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
Matches	16;	Conservative	11; Nismatches	33; Indels	5; Gaps	2;
Oy		1 GLHFIDQHRAAL--TARTVNTVNEWLDALYGVILDEQYQAVRAEPTNPKMRLKLFSPFPA	58	RA	Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	
Db		137 GSQFAEEELRRAFAAYAAMLASLWVPFYSLAFAAVVLSPWMLARSR--QGSKSKLILLVSPC	193	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Jouffard G.G.,	
Oy		59 WNWTC	63	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
Db		194 WGWRG	198	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RESULT 14						
ID	RIK2_HUMAN	STANDARD	PRT	540 AA.	RA	Scheinert A., Schein J.E., Jones S.M., Marria M.A.;
AC	Q43532				RA	"Generation and initial analysis of more than 15,000 full-length
DT	28-Feb-2003	(Rel. 41, Created)			RT	RT human and mouse cDNA sequences";
DT	28-Feb-2003	(Rel. 41, Last sequence update)			RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DT	10-Oct-2003	(Rel. 42, Last annotation update)			CC	-!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
DB	Receptor-interacting serine/threonine protein kinase 2 (ICB 2.7.1.37)				CC	CASP-8-mediated apoptosis. Activates NF-kappaB.
DE	(RIP-1-like interacting CiARP kinase) (Receptor-interacting protein 2)				CC	CATALYTIC ACTIVITY: ATP + a protein = APP + a phosphoprotein.
DE	(RIP-2) (CARD-containing interleukin-1 beta converting enzyme				CC	-!- SUBUNIT: Binds to CiFLAR/CLARP and CiASP1 via their CARD domains.
DE	associated kinase) (CARD-containing interleukin-1 beta converting enzyme				CC	TRAF5. May be a component of both the TNFRSF1A and TNFRSF5/CD40 receptor complex.
OS	Homo sapiens (Human)				CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
OC	Bukaryota; Meczoa; Chordata; Craniata; Vertebrata; Buteleostomi;				CC	-!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung, peripheral blood leukocytes, spleen, kidney, testis, prostate, pancreas and lymph node.
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				CC	-!- PTM: Autophosphorylated.
OX	NCBI_TAXID=9606;				CC	-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
RN					CC	-!- SIMILARITY: Contains 1 CARD domain.
RX	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.,				CC	CC DR AF027706; AAC34970.1; -.
RT	RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CiARP and regulates CD95-mediated apoptosis.";				DR	DR AF078530; AAC27722.1; -.
RL	J. Biol. Chem. 273:12295-12300(1998).				DR	DR AF064824; AAC2568.1; -.
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.				DR	DR AC004303; AAC24561.1; -.
RC	TISSUE=Endothelial cells;				DR	DR AF117829; AAD04634.1; -.
RC	MEDLINE=9307335; PubMed=9642260;				DR	DR BGNC1100420; RLPK2.
RA	McCarthy J.V., Ni J., Dixit V.M.,				DR	DR NM: 603455; -.
RA	"RIP2 is a novel NF-kappaB-activating and cell death-inducing kinase".				DR	DR GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.
RT	RIP-1-like kinase that associates with caspase-1;"				DR	DR GO; GO:0004871; P:signal transducer activity; TAS.
RL	J. Biol. Chem. 273:16968-16975(1998).				DR	DR GO; GO:0006315; P:apoptosis; TAS.
RN	[3] SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.				DR	DR GO; GO:0006354; P:inflammatory response; TAS.
RX	MEDLINE=93031580; PubMed=970538;				DR	DR GO; GO:1000716; P:signal transduction; TAS.
RA	Thome M., Hoffmann K., Burns K., Martonlik F., Bodmer J.-L.,				DR	DR InterPro; IPR001315; Prot kinase.
RA	Matzmann C., Tschoopp J.-J.,				DR	DR InterPro; IPR000719; Prot kinase.
RA	"Identification of CARDIAK, a RIP-like kinase that associates with				DR	DR InterPro; IPR008271; Ser_Ehr_pkink_AS.
RT	Currr. Biol. 8:885-888 (1998).				DR	DR Pfam; PF00619; CARD; 1.
RN	[4] SEQUENCE FROM N.A.				DR	DR Pfam; PF00059; Pkinkase_1.
RA	Ozersky P., Holmes A., Brody M.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.				DR	DR SMART; SM00114; CARD; 1.
RL	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.				DR	DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
RN	[5] SEQUENCE FROM N.A.				DR	DR PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
RA	Platzer M., Varon R., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.				DR	DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
RN	[6] SEQUENCE FROM N.A.				KW	KW Transferase; Serine/threonine-Protein kinase; ATP-binding,
RP	SEQUENCE FROM N.A.				KW	KW Phosphorylation; Apoptosis.
RC	TISSUE=Skin; MEDLINE=22388257; PubMed=12477932;				FT	FT DOMAIN 18 234 PROTEIN KINASE.
RC	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				FT	FT DOMAIN 432 524 CARD.
RA	Klauber R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,				FT	FT BINDING 24 32 ATP (BY SIMILARITY).
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				FT	FT BINDING 47 47 ATP.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsitch F.,				FT	FT ACT_SITE 146 146 K->A: ABOLISHES KINASE ACTIVITY.

FT MUTAGEN 47 47 K->M: REDUCES FAS-MEDIATED APOPTOSIS.
 FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.
 SQ SEQUENCE 540 AA; 61194 MW; 5754692339505792 CRC64;

Query Match 16.5%; Score 62.5; DB 1; Length 540;
 Best Local Similarity 30.4%; Pred. No. 11;
 Matches 17; Conservative 13; Mismatches 23; Indels 3; Gaps 2;

Qy : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 439 WIQSKEEDIVNMTEACLNQSLDAALSRSQJMKPEYLSTKPTSKYRQLLTT 494

RESULT 15
 DX52_RAT DX52_RAT STANDARD PRT; 598 AA.
 ID Q99P70; DT 10-OCT-2003 (Rel. 42, Created)
 AC Q99P70; DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE ROK1-like protein 52 (EC 3.6.1.-) (Putative ATP-dependent RNA helicase
 DE ROK1-like (rROK1).
 GN DDX52 OR ROK1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buthidae; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID:10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Li W, Suzuki T.;
 RT "Identification of a novel ROK1-like protein in rat brain.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 CC -- SUBCELLULAR LOCATION: Nuclear/nucleolar (By similarity).
 CC -- SIMILARITY: Belongs to the DEAD box helicase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; AB055628; BAB32441.1; -.
 DR HSSP; Q58083; IHB8.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00271; helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC_C; 1.
 DR PROSITE; PS00059; DEAD_ATP_HELICASE; FALSE_NEG.
 KW Hydrolase; Helicase; Nuclear Protein; RNA-Binding; ATP-binding.
 FT NP_BIND 210 217 ATP (BY SIMILARITY).
 FT SITE 319 322 DEAD BOX.
 FT DOMAIN 86 92 POLY-LYS.
 SQ SEQUENCE 598 AA; 67239 MW; B9B18EA6B144425 CRC64;

Query Match 16.4%; Score 62; DB 1; Length 598;
 Best Local Similarity 25.0%; Pred. No. 14;
 Matches 26; Conservative 15; Mismatches 19; Indels 44; Gaps 6;
 Qy : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 2 LY-GKVLDEQYQAVRAEPTNPNSKMRKLFSFTPWN---WTCK 64
 26 LY-GKVLDEQYQAVRAEPTNPNSKMRKLFSFTPWN---WTCK 64
 Db 324 LFEDGKTRFDQLASIFLACTSPKVGRAMSATFAYDVEBW-CK 366

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:49:47 ; Search time 28.2289 Seconds

(without alignments)

793.576 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181
Perfect score: 378
Sequence: 1 GLHFDQHRAALIARYTNVE.....LFSFTPANWTCRDLILQLA 71

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315618202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.1*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Result No.	Score	Query	Match	Length	DB ID	Description
1	303	80.2	195	6	Q8HXK9	Q8bxk9 bos taurus
2	269	71.2	193	11	Q8CHX8	Q8chx8 rattus norvegicus
3	73.5	19.4	220	11	Q8C550	Q8c550 mus musculus
4	69.5	18.4	220	11	Q8R2S3	Q8r2s3 mus musculus
5	68	18.0	449	16	Q8BNWC4	Q8bnwc4 lactobacillus
6	68	18.0	545	16	Q9CBU2	Q9cbu2 mycobacterium
7	67	17.7	257	4	Q9H695	Q9h695 homo sapiens
8	67	17.7	912	15	Q9O278	Q9o278 chimpanzee
9	67	17.7	1175	16	Q8XNW6	Q8xnw6 clostridium
10	66.5	17.6	1170	16	Q8B2B7	Q8b2b7 pseudomonas
11	66	17.5	249	4	Q8N528	Q8n528 homo sapiens
12	65.5	17.3	149	16	Q8FTY0	Q8fty0 cornebacterium
13	65.5	17.3	616	13	Q804E2	Q804e2 dictyurus
14	65.5	17.3	628	13	Q8UWD2	Q8uwd2 brachydanio
15	65	17.3	647	13	Q7TOK2	Q7tok2 brachydanio
16	65	17.2	1134	16	Q8PEL2	Q8pel2 xanthomonas

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	303	80.2	195	6	Q8HXK9	Q8bxk9 bos taurus
2	269	71.2	193	11	Q8CHX8	Q8chx8 rattus norvegicus
3	73.5	19.4	220	11	Q8C550	Q8c550 mus musculus
4	69.5	18.4	220	11	Q8R2S3	Q8r2s3 mus musculus
5	68	18.0	449	16	Q8BNWC4	Q8bnwc4 lactobacillus
6	68	18.0	545	16	Q9CBU2	Q9cbu2 mycobacterium
7	67	17.7	257	4	Q9H695	Q9h695 homo sapiens
8	67	17.7	912	15	Q9O278	Q9o278 chimpanzee
9	67	17.7	1175	16	Q8XNW6	Q8xnw6 clostridium
10	66.5	17.6	1170	16	Q8B2B7	Q8b2b7 pseudomonas
11	66	17.5	249	4	Q8N528	Q8n528 homo sapiens
12	65.5	17.3	149	16	Q8FTY0	Q8fty0 cornebacterium
13	65.5	17.3	616	13	Q804E2	Q804e2 dictyurus
14	65.5	17.3	628	13	Q8UWD2	Q8uwd2 brachydanio
15	65	17.3	647	13	Q7TOK2	Q7tok2 brachydanio
16	65	17.2	1134	16	Q8PEL2	Q8pel2 xanthomonas

SEQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
RP MEDIATYPE=2056038; PubMed=10567338;
RX PMID=1036508;
RA Masumoto J., Taniguchi S., Ayukawa K., Sarvorham H., Kishino T.,
RA Katsuyama T., Sagara J., Hidaka J.Y., Hidaka P.,
RA Postlethwait J.H., Nunez G., Inohara N.;
RT "Caspy: A zebrafish caspase activated by ASC oligomerization required
for pharyngeal arch development.";
RN NCBI_TaxID=9913;
RN J. Biol. Chem. 0:0-0(2002).
RN SEQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
RP MEDIATYPE=2056038; PubMed=11139337;
RX PMID=1139337;
RA Masumoto J., Taniguchi S., Ayukawa K., Sagara J.;
RT "Marine ortholog of ASC, a CARD-containing protein, self-associates,
and exhibits restricted distribution in developing mouse embryos.";
RT EXP.; Cell Res. 262:128-133(2001).
DR ENZYME: AB05006; BAC41353.1;
DR GO:GO:0005622; C:intracellular, IEA.

QY	57 ----- PAWN 61	Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skeilton J., Squares R., Stevens S., Taylor K., Whitehead S., Woodard J.R.,
Db	72 ACQELLRCACQTVMPDPADW 93	
		RA RA RA RA RA RA
		Rutte S., Seeger K., Simon S., Simmonds M., Skeilton J., Whitehead S., Woodard J.R.,
		Squares S., Stevens S., Taylor K., Whitehead S., Woodard J.R.,
		RA RA RA RA RA RA
		Barrell B.G.; RT RT RT RT RT RT
		"Massive gene decay in the leprosy bacillus"; Nature 401:1007-1011 (2000); RL RL RL RL RL RL
		EMBL; AL581923; CAC30769.1; -
		DR PIR; A87136; A87136.
		DR PIRoma; ML1816; -
		DR GO; GO:0016020; C:membrane; IEA.
		DR GO; GO:0005524; F:ATP binding; IEA.
		DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . . ; IEA.
		DR GO; GO:0001166; :nucleotide binding; IEA.
		DR GO; GO:0006810; P:transport; IEA.
		DR InterPro; IPR003593; AAA ATPase.
		DR InterPro; IPR003439; ABC Transporter.
		DR Pfam; PF00005; ABC tran.; 2.
		DR Prodrom; PD000006; ABC transporter; 2.
		DR SMART; SM00382; AAA; 2.
		DR PROSITE; PS00211; ABC TRANSPORTER_1; 2.
		DR PROSITE; PS50893; ABC TRANSPORTER_2; 2.
		XW ATP-binding; Complete_protein; IEA.
		SEQUENCE 545 AA; 58986 MW; 75AAA463EB91BCD CRC64;
		SQ
		Query Match 18.0%; Score 68; DB 16; Length 545;
		Best Local Similarity 36.4%; Pred. No. 9.7;
		Matches 20; Conservative 3; Mismatches 16; Indels 16; Gaps 2;
		Qy 8 HRAALIARVTVNEWLDALYGVK-----LTD EQYQAVRAEFTNPNSK 48
		Dd 226 HNVELTAAVNVRWFDAVLGKVDFYNNMGRKYLLDSRATDEQRR-RRERVNAER 278
		RESULT 7
		Q9H695 PRELIMINARY; PRT; 257 AA.
		AC Q9H695 ID Q9H695
		DT 01-MAR-2001 (TrEMBLrel. 16, Created)
		DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
		DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
		DE Hypothetical protein FLJ22474.
		OS Homo sapiens (Human).
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		NCBI_TaxID=9606; [1]
		RN SEQUENCE FROM N.A.
		RP Kawabata A., Hiraki T., Kobatake N., Inagaki H., Ikemoto Y., Okamoto S., Oikitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S., RT RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
		RL DR Genew; HGNC:120310; GRTPL.
		DR GO; GO:0005576; C:extracellular; IEA.
		DR GO; GO:0005179; F:homologous protein activity; IEA.
		DR InterPro; IPR000195; RabGAP TBC.
		DR InterPro; IPR0001400; SomatoTropin.
		DR Pfam; PF00566; TBC; 1.
		DR SMART; SM00164; TBC; 1.
		DR PROSITE; PS003338; SOMATOTROPIN 2; 1.
		DR PROSITE; PS50086; TBC_RABGAP; 1.
		XW Hypothetical Protein.
		SEQUENCE 257 AA; 28960 MW; 5B0A7E5779DFF2B94 CRC64;
		SQ
		Query Match 17.7%; Score 67; DB 4; Length 257;
		Best Local Similarity 33.9%; Pred. No. 5.2;
		Matches 19; Conservative 10; Mismatches 19; Indels 8; Gaps 2;
		Qy 1 GLHFIDQHRAALIARVTVNEWLDALYGVK-----LTD EQYQAVRAEFTNPNSKMRKL 52
		Dd 69 GRNFN----AGFLVLIINNEEESSWLDALYGRILFDYYSFAMLGKTDQEVGLGEL 120
		NCBI_TaxID=1769; [1]
		RN SEQUENCE FROM N.A.
		RC RC RC RC RC RC
		TN MEDLINE=21128732; PubMed=11234002;
		RA Cole S.T., Eigemeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Maclean J., Lacroix C., Moule S.,
		RA RA RA RA RA RA

PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS00290; IG_MHC; 1.

DR PROSITE; PS00015; MITOCH_CARRIER; 1.

DR PROSITE; PS50110; RESPONSE_REGULATOR_Y; 3.

KW Kinase; Complete proteome.

SEQUENCE 1170 AA; 131102 MW; 8C649FC4DC65B05B CRC64;

Query Match 17.6%; Score 65.5; DB 16; Length 1170;

Best Local Similarity 24.6%; Pred. No. 38; Indels 10; Mismatches 16; Conservative 1; Matches 16; Gaps 1;

Qy 3 HFIDQHRAALIARYTNVNLDDALIGKVLTDEQYQAVRAEPTNPKRKLFSFTPAWNWT 62

Db 82 HFIDQHRAALIARYTNVNLDDALIGKVLTDEQYQAVRAEPTNPKRKLFSFTPAWNWT 62

Qy 63 CKDIL 67

Db 129 AQDMI 133

RESULT 11

Q8N728 PRELIMINARY; PRT; 249 AA.

ID Q8N728; AC Q8N728; DT 01-OCT-2002 (TREMBLrel. 22, Created) DT 01-JUN-2002 (TREMBLrel. 22, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DB Similar to hypothetical protein FLJ22474.

OS Homo sapiens (Human).

EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI TAXID=9606;

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RA Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; BCO33071; AAH33071.1; -.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005179; P:hormone activity; IEA.

DR InterPro; IPR00195; RadGAP_TBC.

DR InterPro; IPR001400; Somatotropin.

PFam; PF00566; TBC; 1.

DR SMART; SM00164; TBC; 1.

PROSITE; PS00338; SOMATOTROPIN_2; 1.

DR PROSITE; PS50086; TBC_RABGAP; 1.

KW Hypothetical protein.

SEQUENCE 249 AA; 28446 MW; 49B1FB8607705438 CRC64;

Query Match 17.5%; Score 66; DB 4; Length 249;

Best Local Similarity 33.9%; Pred. No. 6.7; Indels 8; Gaps 2;

Matches 19; Conservative 10; Mismatches 19; Hypothetical protein.

Qy 1 GLHFIDQHRAALIARYTNVNLDDALIGKVLTDEQYQAVRAEPTNPKRKLFSFTPAWNWT 52

Db 69 GMNFI--AGYLILITNNBEEFWILDALVGRILLPDYYSPEMLGLKTIDQEVLGEL 120

RESULT 12

Q8FTY0 PRELIMINARY; PRT; 149 AA.

ID Q8FTY0; AC Q8FTY0; DT 01-MAR-2003 (TREMBLrel. 23, Created) DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

GN CE043.

OS Corynebacterium efficiens. Actinobacteridae; Actinomycetales; Bacteria; Actinobacteria.

OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

NCBI TAXID=152794;

RN [1]

SEQUENCE FROM N.A.

RP

RC STRAIN=Y5-314 / AJ 12310 / DSM 44549 / JCM 11189; RA Kawarabayashi Y.; Yamazaki J.; Hino Y.; Kikuchi H.; Nakamura Y.; Iikeo K.; Suzuki M.; Mashima J.; Itoh T.; Yamagishi A.; Niishio Y.; Usuda Y.; Sugimoto S.; RA "The entire genomic sequence of Corynebacterium efficiens YS-314." RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR AP005214; BAC17053.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 149 AA; 16334 MW; D1.861ADB491A4 F5 CRC64;

Query Match 17.3%; Score 65.5; DB 16; Length 149;

Best Local Similarity 32.7%; Pred. No. 4.1; Indels 3; Gaps 2;

Matches 17; Conservative 11; Mismatches 21; Hypothetical protein.

Qy 7 QHRAALIARYTNVNLDDALIGKVLTDEQYQAVRAEPTNPKRKLFSFT 56

Db 99 QHSKASIAASRTELSHIWISASYTQLAD-TYSVIFADDMENIARRETWT 149

RESULT 13

Q804B2 PRELIMINARY; PRT; 616 AA.

ID Q804B2; AC Q804B2; DT 01-JUN-2003 (TREMBLrel. 24, Created) DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR AA024632.1; -.

DE Inhibitor of apoptosis protein-1.

GN CIAP-1.

OS Ictalurus punctatus (Channel catfish).

EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.

NCBI TAXID=7998;

RN [1]

RP

SEQUENCE FROM N.A.

RA Praveen K.; Leary J.H.; III; Evans D.L.; Jaso-Friedmann L.; Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

RT "Cloning of anti-apoptotic genes in non-specific cytotoxic cells."

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR AA184337; AA024632.1; -.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:000518; P:apoptosis inhibitor; IEA.

DR GO; GO:0005916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00053; BIR; 3.

DR Pfam; PF000619; CARD; 1.

DR Pfam; PF00097; Zf-CSHC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00194; RING; 1.

DR PROSITE; P501282; BIR_REPEAT_1; 2.

DR PROSITE; P501043; BIR_REPEAT_2; 3.

DR PROSITE; P502009; ZF_RING; 2; 1.

DR PROSITE; P500089; ZF_RING; 2; 1.

SEQNCE 616 AA; 69546 MW; D1389D915C6BB256 CRC64;

Query Match 17.3%; Score 65.5; DB 13; Length 616;

Best Local Similarity 34.1%; Pred. No. 23; Indels 1; Gaps 1;

Matches 14; Conservative 12; Mismatches 14; Hypothetical protein.

Qy 1 GLHFIDQHRAALIARYTNVNLDDALIGKVLTDEQYQAVRAEPTNPKRKLFSFT 40

Db 455 GFTFLKGHHAULTQRLKSVQLSMDHLEENVISQKEYDTIR 495

RESULT 14

Q8WUD2 PRELIMINARY; PRT; 628 AA.

ID Q8WUD2; AC Q8WUD2; DT 01-MAR-2002 (TREMBLrel. 20, Created) DT 01-MAR-2003 (TREMBLrel. 20, Last sequence update)

DR

DE Iapi.
 GN IAPI.
 Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBITaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373732; PubMed=10917738;
 RA Inohara N.; Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in
 zebrafish."
 RL Cell Death Differ. 7:509-510 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inohara N.; Nunez G.;
 RL Submitted 'NOV-2001' to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AF442500; AAI33679; 1.
 DR GO: GO:005622; C:Intracellular; IEA.
 DR GO: GO:0005189; F:Apoptosis inhibitor activity; IEA.
 GO: GO:0006916; P:Anti-apoptosis; IEA.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001370; CARD.
 DR InterPro; IPR001841; Znf_finger.
 DR Pfam; PF00653; BIR; 3.
 DR Pfam; PF00619; CARD; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Metal-binding; Zinc-finger.
 SQ 628 AA; 70098 MW; 5B6CEB6A87C8A9 CRC64;
 Query Match 17.3%; Score 65.5%; DB 13; Length 628;
 Best Local Similarity 34.1%; Pred. No. 24;
 Matches 14; Conservative 13; Mismatches 13; Indels 1; Gaps 1;
 Qy 1 GLIFIDQHARLIAARYTINWELLDALYK-VLTDEQIQA9 40
 Db 467 GFTFLRKHHAAALSQRKSVQSLMDHLEENVISQKEYDSDIR 507

RESULT 15

QTOK2 ID QTOK2 PRELIMINARY; PRT; 647 AA.
 AC Q7T052;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Inhibitor of apoptosis protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBITaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Enz K.M.; Valdimarsson G.;
 RT "Zebrafish inhibitor of apoptosis protein."
 RL Submitted 'MAR-2003' to the EMBL/GenBank/DDBJ databases.
 DR EMBL:AY247786; AAC04493; 1;-
 SQ SEQUENCE 647 AA; 72183 MW; 88DBBAFB92718FA9 CRC64;

Query Match 17.3%; Score 65.5%; DB 13; Length 647;
 Best Local Similarity 34.1%; Pred. No. 25;
 Matches 14; Conservative 13; Mismatches 13; Indels 1; Gaps 1;